

ALK-5

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu Jun 26 04:11:00 1997; MasPar time 1905.03 Seconds
Tabular output not generated. 1347.129 Million cell updates/sec
Title: >US-08-436-265-9
Description: (1-2308) from US08436265.seq
Perfect Score: 2308
N.A. Sequence: 1 GCGAGGCGAGGTTTGCTGG.....TGTTAAACCTATAGTGT 2308
Comp: CCGCTCCGCTCCAAACGACC.....ACAATTTGGATATCACAAA

Scoring table: TABLE default
Gap 6
Nmatch: STD : Dbase 0; Query 0
Search: 333249 seqs, 555961234 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

emb1-new11
1:BCT 2:FUN 3:GEN 4:HUM 5:SUM 6:HUM3 7:INV1 8:INV2
9:INV3 10:INV4 11:INV5 12:INV6 13:INV7 14:ORG 15:MAM
16:VRT 17:PLN 18:PRO1 19:PRO2 20:ROD 21:SYN 22:UNC
23:VIR1 24:VIR2
genbank97
25:BCT1 26:BCT2 27:BCT3 28:BCT4 29:BCT5 30:BCT6 31:BCT7
32:BCT8 33:BCT9 34:GEN1 35:GEN2 36:HTG 37:INV1 38:INV2
39:INV3 40:INV4 41:INV5 42:INV6 43:INV7 44:INV8 45:INV9
46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3 52:PAT1
53:PAT2 54:PAT3 55:PAT4 56:PHG 57:PLN1 58:PLN2 59:PLN3
60:PLN4 61:PLN5 62:PLN6 63:PLN7 64:PLN8 65:PLN9 66:PLN10
67:PRI1 68:PRI2 69:PRI3 70:PRI4 71:PRI5 72:PRI6 73:PRI7
74:PRI8 75:PRI9 76:PRI10 77:PRI11 78:PRI12 79:PRI13
80:PRI14 81:ROD1 82:ROD2 83:ROD3 84:ROD4 85:ROD5 86:ROD6
87:ROD7 88:ROD8 89:STR 90:SYN 91:UNA 92:VRL1 93:VRL2
94:VRL3 95:VRL4 96:VRL5 97:VRL6 98:VRL7 99:VRL8 100:VRL9
genbank-new11
101:BCT 102:GEN 103:INV1 104:INV2 105:MAM 106:VRT
107:PHG 108:PLN 109:PRI1 110:PRI2 111:ROD 112:SYN
113:UNA 114:VRL
Database: u-emb148_97
Statistics: Mean 12.312; Variance 5.693; scale 2.085

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Match	Length	ID	Description	Pred. No.
1	2308	100.0	2308	75	HUMALK5A Human activin recepto	0.00e+00
2	1253	54.3	2860	86	MUSTGFB1R Mouse mRNA for TGF-be	0.00e+00
3	1221	52.9	1381	47	MSU37065 Mustela sp. TGF-b typ	0.00e+00
4	1150	49.8	1659	20	MMTGFBPTI Mouse mRNA for TGF-be	0.00e+00
5	1150	49.8	1659	86	MUSTGFB1R Mouse mRNA for TGF-be	0.00e+00
6	1102	47.7	1506	55	123851 Sequence 4 from paten	0.00e+00
7	1102	47.7	1506	85	125010 Sequence 4 from paten	0.00e+00
8	1102	47.7	1545	87	RA1SETHK1R Rat transforming grow	0.00e+00
9	833	36.1	2186	49	CHKRPK2 Chicken RPK-2 mRNA fo	0.00e+00
ALIGNMENTS						

RESULT 1

LOCUS HUMALK5A 2308 bp mRNA PRI 24-JAN-1994
DEFINITION Human activin receptor-like kinase (ALK-5) mRNA, complete cds.
ACCESSION L11695
NID 9431034
KEYWORDS activin; activin receptor-like kinase; serine/threonine kinase; transforming growth factor-beta; transmembrane protein.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2308)
AUTHORS Franzen,P., ten Dijke,P., Ichijo,H., Yamashita,H., Schulz,P., Heldin,C.H. and Miyazono,K.
TITLE Cloning of a TGF beta type I receptor that forms a heteromeric complex with the TGF beta type II receptor
JOURNAL Cell 75 (4), 681-692 (1993)
MEDLINE 94061986

Query Match 100.0%; Score 2308; DB 75; Length 2308;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 2308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
LOCUS MUSTGFB1R 2860 bp mRNA ROD 04-OCT-1994
DEFINITION Mouse mRNA for TGF-beta type II receptor, complete cds.
ACCESSION U37065
NID 9483375
KEYWORDS TGF-beta type I receptor; serine/threonine kinase receptor; transforming growth factor-beta type I receptor.
SOURCE Mus musculus brain cDNA.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2860)
AUTHORS Suzuki,A., Shiota,N., Maeda,T., Tada,M. and Ueno,N.
TITLE A mouse TGF-beta type I receptor that requires type II receptor for ligand binding
JOURNAL Biochem. Biophys. Res. Commun. 198 (3), 1063-1069 (1994)
MEDLINE 94161715

Query Match 54.3%; Score 1253; DB 86; Length 2860;
Best Local Similarity 89.0%; Pred. No. 0.00e+00;
Matches 1537; Conservative 0; Mismatches 170; Indels 19; Gaps 11;

RESULT 3
LOCUS MSU37065 1381 bp mRNA MAM 31-OCT-1995
DEFINITION Mustela sp. TGF-b type I receptor mRNA, partial cds.
ACCESSION U37065
NID 91045609
KEYWORDS mink.
SOURCE ORGANISM Mustela sp.
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
REFERENCE 1 (bases 1 to 1381)
AUTHORS Weis-Garcia,F. and Massague,J.
TITLE Complementation between kinase-defective and activation-defective TGF-beta receptors reveals a novel form of receptor cooperativity
JOURNAL EMBO J. (1995) In press
REFERENCE 2 (bases 1 to 1381)
AUTHORS Weis-Garcia,F.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-1995) Frances Weis-Garcia, Cell Biology &

RESULT 4
ID MMTGFBPTI standard; RNA; ROD; 1659 BP.
AC D28526;
NI 9467521

291	Db	ggatcactgcaataaaatagaaactcccaactacaggaccttttcagaaaaagcagtcagc	350
375	Qy	GCTGCAAT-CAGGACCATTCGATATAAATAGA-ACTTCCAACACTACTGTAAGTATCATCACC	432
351	Db	tggcctcggctcgtggaagctggcagctgtcattgctgggtccagtcctgcttcgctctgcat	410
433	Qy	TGGCCTTGGTCCTGTGGAACGGCAGCTGTCAATGCTGGACAGAGTGTGCTTCGCTCGCAT	492
411	Db	tgcacttatgctgatggtctctatatctgccataaacgcgcaactgtcattcacaccgcggtgcc	470
493	Qy	CTCACTCATGTTGATGGTCTATATCTGCACAAACCGCACTGTCAATTCACCATCGAGTGCC	552
471	Db	aaatgaagaggatccctcactagatgcgcctttcatttcagaggccaccaccttaaaga	530
553	Qy	AAATGAAGAGGACCTTCATTAGATCGACCTTTTATTTCAGAGGGTACTACGTTGAAAGA	612
531	Db	tttaatttatgatgatgacaacatcagggtctgcatcaggttttacacactctgtttcaag	590
613	Qy	CTTAATTTATGATATGACAACGCTCAGGTTCTGGCTCAGGTTTACCATTTGTTTTCAGAG	672
591	Db	aacaattgcaagaccattgtgtctacafaaagcatcggcgaaggtcgggtttgggagaagt	650
673	Qy	AACAAATGGCAGAACTATTGTGTACAGAAAGCAATTTGGCAAGGTGATTTGGAGAAAT	732
651	Db	tggcgaggcaaatggcgggagaaagaagttgcgctgaagatatctctctctagagaaga	710
733	Qy	TTGGAGAGGAAAGTGGCGGGAGAGAAAGTTGCTGTTAAGATATTCTCTCTAGAGAAGA	792
711	Db	acgtttcatggttccgagaggcagaagatttatcagactgtaattgtttacgcccataaataat	770
793	Qy	ACGTTTCGTGGTCCGTGAGGCAGTCTTAATAAACTGTAATGTTACGTCATGAAACAT	852
771	Db	cctgggggtttatagcagcagacaaacaaagaaatggtacatggagctcagctgtgggttgg	830
853	Qy	CCTGGGATTTATAGCAGCAGACAATAAAGACATGTTACTTTGGACTCAGCTCTGGTTGTT	912
831	Db	gtcggattatcatgagcatggatcccttttcgattacttgaatagatcacactgttactgt	890
913	Qy	GTCAGATTATCATGAGATGGATCCCTTTTGTGATTACTTAACAGATACACAGTTACTGT	972
891	Db	ggaaggaatgatcaaatcgctctgtccacggcaagtgggtcttgcccatcttcacatgga	950
973	Qy	GGAGGAATGATAAAACTTGCTCTGTCCACGGCGAGCGGTCTTGCCCATCTTCACATGGA	1032
951	Db	gattgttggtaccagaaacacgacttatgcccataagagatttgaatacaagaatat	1010
1033	Qy	GATTGTTGGTACCAAGAAAGCCAGCCATTGCTCTATAGAGATTTGAAATCAAGAATAT	1092
1011	Db	cttgggtgaagaaaaatggaacctgtgtattgacagatttgggacttgcgtgacagcatga	1070
1093	Qy	CTTGTAAGAAGAAATGSAACTTGCTGTAATTGACAGATTAGGACTTGGCAGTAAGACATGA	1152
1071	Db	tcttgccacagatacaattgatattgctccaaacacagagtaggcataaaaggtatat	1130
1153	Qy	TTCAAGCCACAGATACCAATTGATATTGCTCCAAACACAGAGTGGGAAACAAAAGGTACAT	1212
1131	Db	ggcccttgaagttctagatgattccataaataatgaaacattttgaatccttcaaacgtgc	1190
1213	Qy	GGCCCTTGAAGTCTTCGATGATTTCATAAATATGAAACATTTTGAATCCTTCAACAGTGC	1272
1191	Db	tgaatctatgaaatgggcttagtattctgggaaatcgctcgacgctgttccattggcg	1250
1273	Qy	TGACATCTATGCAATGGGCTTAGTATTCTGGGAAATTTGCTCGACGATGTTCCATTGGTGG	1332
1251	Db	aatccacgaagactaccagttgccttactatgatctgtaccttctgacccatccogttga	1310
1333	Qy	AATTCATGAAGATTACCACTGSCCTTTATTATGATCTTGTAACCTTGTGACCAATCAGTTGA	1392
1311	Db	agaaatgagaaaaagtgttgtgaacagaagtaaggcccaaatattcccaacagatggca	1370
1393	Qy	AGAAATGAGAAAAGTTGTTTGTGAACAGAAAGTTAAGGCCAAATATCCCAAAACAGATGGCA	1452

Db 1371 gagctgtgagccttgagagtgatggcacaattatgagagaattgttgatgccaatgg 1430
Qy 1453 GAGCTGTGAAGCCTTGAGAGTAATGGCTAAATATGAGAGAAATGTTGGTATGCCAATGG 1512
Db 1431 agcagtaggtgacagcttgcgaatcaaaaaacattgcacagctcagccaacagga 1490
Qy 1513 AGCAGTAGGCTTACAGCATTCGGGATTGAAGAAAACATTTATCGCAACTCAGTCAACAGGA 1572
Db 1491 aggcatacaaatgtaa 1506
Qy 1573 AGGCATCAAAATGTAA 1588
RESULT 7 125010 1506 bp DNA FAT 21-AUG-1996
LOCUS Sequence 4 from patent US 5547854.
ACCESSION 125010
NID 91604880
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1506)
DONAHOE, P.K., Gustafson, M. and He, W.W.
DNA encoding a receptor for Mullerian inhibitory substance, misr1,
and corresponding vectors, cells, probes, and recombinant methods
JOURNAL Patent: US 5547854-A 4 20-AUG-1996;
FEATURES
source 1..1506
Location/Qualifiers
BASE COUNT 428 a 321 c 363 g 394 t
ORIGIN
Query Match 47.7%; Score 1102; DB 55; Length 1506;
Best Local Similarity 88.9%; Pred. No. 0.00e+00;
Matches 1294; Conservative 0; Mismatches 156; Indels 6; Gaps 5;
Db 51 ggtggcggcgagcgtgctccggggggcgaaggcattacagtggtttctgcccactctg 110
Qy 139 GCGGCGCGCGCGCGCTGCTCCGCGGGCGACGCGGTTACAGTGTTCGCGCACCTCTG 198
Db 111 tacaaggacaattttacttgtgagacayatggtctctgcttctgctcagtcacagagac 170
Qy 199 TACAAAAGACAATTTTACTTGTGTGACAGATGGGCTCTGCTTGTCTCTGTCCACAGAC 258
Db 171 cacagacaagtatacacaatagcatgtgtatagctgaatcgacacctaattccccgaga 230
Qy 259 CACAGACAAGCTTATACACAACAGCATGTGTATAGCTGAATGACTTAATTCCTCGAGA 318
Db 231 caggccatttgttgccaccattctcaaaaacaggggcgagttacgtattgtctgcaatca 290
Qy 319 TAGGCCGTTGTATGTGCACCCCTCTCAAAAACCTGGTCTGTGAC--ATT- 374
Db 291 ggaatcactgcaataaaatagaactcccaactcagagacctttttcagaanaagcagtcagc 350
Qy 375 GCTGCAAT-CAGGACCATTGCAATAAATAGA-ACTTCCAACACTACTGTAAAGTCATCACC 432
Db 351 tggcctcggtcctgtgagagctggcagctgtcattgtggtccagctgtgctctgcat 410
Qy 433 TGGCCTTGGTCTGTGGAACCTGGCAGCTGTCTAATGCTGGACCAGTGTGCTTCTGCTGCAT 492
Db 411 tgcacttatgctgagtggtctatatctcgccataacgcagcactgtcattcaccaccgggtgcc 470
Qy 493 CTCACACTATGTTGATGGTCTATATCTGCCACAACCGCACTGTCTATTACCATCGAGTGCC 552
Db 471 aaatgaaggaggtccctcactagatcgcccttttctatttcagagggccaccaccttaaaaga 530
Qy 553 AAATGAAGAGGACCCCTTCATTAGATCGCCCTTTTATTTCAGAGGGGTACTACGTTGAAAGA 612
Db 531 tttaatttatgatgacaacatcagggtctggatcaggtttaccactgctgtgtcaaaag 590

Qy 613 CTTAAATTATGATATGACAACGTCAGGTTCTGGCTCAGGTTTACCATTGCTGTTTCAGAG 672
Db 591 aacaattgcaaggaccattgtgtacaagaagcatcggaaggctcggtttggagaagt 650
Qy 673 AACAAATGCGAAGCACTATGTGTTTACAGAAAGCATTTGGCAAAGGTCGATTGGAGAAGT 732
Db 651 ttggcgaggcaaatggcgggggagagaagttcgcggtgaagatatctctctctagagaaga 710
Qy 733 TTGGAGAGGAAGTGGCGGGGAGAGAAGTTGCTGTTTAAAGATATTCTCCTCTAGAGAAGA 792
Db 711 agtttcattggttccgagaggcagagatttatcagactgtaattgttacgcaatataat 770
Qy 793 AGCTTCGTGTTCCGTGAGGACAGAGATTATCAAACTGTAACTGTAATGTTACGTCATGAAAACAT 852
Db 771 cctgggggtttatagcagcagacaacaagaacaaatggtlacatggactcagctggttgggt 830
Qy 853 CCTGGGATTTATAGCAGCAGACAATAAAGACAATGGTACTTGGACTCAGCTCTGGTTGGT 912
Db 831 gtcggattatcatgagcatggtatcccttttcgattacttgaatagatatacaactgttactgt 890
Qy 913 GTCAGATTATCATGAGCATGGATCCCTTTTGTATTACTTAAACAGATACACAGTTACTGT 972
Db 891 ggaaggaatgatcaaaactcgctctgtcccaggcaagtggtcttggccactcttcacatgga 950
Qy 973 GGAAGGAATGA7AAAACTTGCTCTGTCTGTC773GGCGAGCGGCTTTGCCCACTTTCACATGGA 1032
Db 951 gattgttggtaccgaaggaaaaaccagctattggccatagagatttgaatatcaagaatat 1010
Qy 1033 GATTGTTGTTACCCAAGGAAGCCAGCCATTGCTCATAGAGATTTGAAATCAAGAATAT 1092
Db 1011 cttggtgaagaaaaatggaacctgtgtattgcagatttgggacttgcgtgagacatga 1070
Qy 1093 CTTGGTAAAGAGAAATGGAACCTTGCTGTATTGAGACTTAGGACTGGCAGTAGACATGA 1152
Db 1071 ttctgcccacagatcaaatgtattgttctccaaaccacagagtaggactcaaaaggtatat 1130
Qy 1153 TTCAGCCACAGATACCAATGTGATTTGCTCCAAACCACAGAGTGGGAACAAAAGGTACAT 1212
Db 1131 ggcacctgaagttcttagatgattccataataatgaacacatttggaaatccttcaaacgtgc 1190
Qy 1213 GGCCCTCGAAGTTCTCGATGATTCATCAATAATATGAACATTTTGAATCCTTCAACGTCG 1272
Db 1191 tgacattctatgcaatggccttagtattctgggaaatcgctcgagctgttccattggcgg 1250
Qy 1273 TGACATCTATGCATGGCTTAGTATTCTGGGAAATGCTCGACGATGTTCCATTGGTGG 1332
Db 1251 aatccacgaaagactaccagttgaccttactatgacttctgtacctctctgacctccgttga 1310
Qy 1333 AATTCATGAAGATTACCAACTGCCTTATTATGATCTTTGTACCTTCTGACCCATCAGTTGA 1392
Db 1311 agaaatgagaaaaagtagtttgtgaacagaagtttaaggccaaatattcccaacagatggca 1370
Qy 1393 AGAAATGAGAAAAGCTTGTGTTGTGAACAGAAAGTTAAGGCCAAATATCCCAACAGATGGCA 1452
Db 1371 gagctgtgagccttggagagtgatggccaaaataattatgagagaatggttggtatgccaatgg 1430
Qy 1453 GAGCTGTGAAGCCCTTGAGAGTAATGSGCTAAATTTATGAGAGAAATGTTGGTATGCCAATGG 1512
Db 1431 agcagctaggctgacagcttgcgaattaaaaaaacatttcacagctcagccaacagga 1490
Qy 1513 AGCAGCTAGGCTTACAGCATTCGGGATTGAAGAAAACATTTATCGCAACTCAGTCAACAGGA 1572
Db 1491 aggcatacaaatgtaa 1506
Qy 1573 AGGCATCAAAATGTAA 1588
RESULT 8
LOCUS RATSETHKIR 1545 bp mRNA ROD 11-DEC-1995
DEFINITION Rat transforming growth factor beta type I receptor mRNA, complete

390 tggcctcgtgctgtggagctggcagctgtcattgctggtccagctgtctctcgtcat 449
433 TGGCCTTGGTCTCTGTGGAACCTGGCAGCTGTCATTGCTGGACCGAGTGTCTTCTGTCAT 492
450 tgcacttatgtgtgcttatctatctgccaataaacgcactgtcattcaccaccgctgccc 509
493 CTCACATCATGTTGATGGTCTATATCTGCCACAACCGCACTGTCTTACCATCCAGTGCC 552
510 aaatgaagagagatccctcactagatcgccctttcatttcagagggcaccaccttaaaaga 569
553 AAATGAAGAGAGACCTTCTATTAGATCGCCCTTTTATTTCAGAGGGTACTACGTTGAAGA 612
570 ttttaattatgatgacacaacatcagggtctggtatcaggtttaccactgcttcttcaag 629
613 CTTAAITTTATGATATGACAACGTGAGTCTGGCTCAGTTTACCATTGCTTGTTCAGAG 672
630 aacaattgcaggaccattgtgtctacaagaagcatcggaagagtcggttttgagagagt 689
673 AACAAITGCGAGAATCTATTGCTTACAAGAAAGCATTTGGCAAAGTTCGATTTGGAGAAGT 732
690 ttggcgaggcaaatggcggggagagaagtgcgcgtgaagatatctctctcttagagaaga 749
733 TTGGAGAGGAAAGTGGCGGGGAGAGAAGTTGCTGTGTAAGATATTTCTCTCTAGAGAAGA 792
750 acgttcattggttcgagagagcagagatttatcagactgtaattgttacgccaataaatat 809
793 ACGTTCGTGTTCCGTGAGGAGAGATTTATCAAACTGTAATGTTACGTCATGAAAACAT 852
810 cctgggggtttatagcagcagacaacaagaacatggtacatggtcagctcagctgtggttgg 869
853 CCTGGGATTTATAGCAGCAGACAATAAGACAATGGTACTTGGACTCAGCTCTGTTGGT 912
870 gtgcgattatcatgagcagtggtgctccttttcgatttacttgatgaatagatacactgttactgt 929
913 GTCAGATTTATCATGAGCATGGATCCCTTTTGTATTACTTTAAACAGATACAGTTACTGT 972
930 ggaagaaatgatcaaatcgctcgtccagggcaagtggtcttgcccatcttcacatgga 989
973 GGAAGGAATCATAAACTTGTCTGTCTCCAGCGGAGGGTCTTGCCCATCTTCCATGGA 1032
990 gattgtgtgaccagaagaaaccagctattgcccataagagattggaatacaagaatat 1049
1033 GATTGTGTTACCAAGAAAGCCAGCCATTTGCTCATAGATTTGAAATCAAGAAATAT 1092
1050 cttggtggaagaaaaatggaacctgtgtattgagatttgggaactgtgtgtgagacatga 1109
1093 CTTGGTAAAGAAAGAAATGGAACCTGCTGTATTGACAGCTTAGGAGTGGCAGATGA 1152
1110 ttctgcccagatacaattgtatattgctccaaaccacagagtaggcaataaaggtatat 1169
1153 TTCAGCCACAGATACCATTTGATTTGCTCCAAACCACAGAGTGGGAACAAAAGGTACAT 1212
1170 ggccctggaagttctatagatccataaatgaaacattttgaatccttcaacgtgc 1229
1213 GGGCCCTGGAAGTTCTCGATGATTCCTCAATAATATGAACAATTTTGAATCTTCAACGTGC 1272
1230 tgacatctatgcaatggccttagtattctgggaaatcgctcagcgtgttccatggcgg 1289
1273 TGACATCTATGCAATGGCTTAGTATTCTGGGAAATTTGCTCGACGATGTTCCATTGGTGG 1332
1290 aatccacgaagactaccagttgccttactatgatcttctgtaccttctgtatccatcggtga 1349
1333 AATTCAATGAAGATTACCAACTGCCCTTATTATGATCTTGTACTTCTGACCCCAACAGTTGA 1392
1350 agaaatgagaaaaagtagttgtgaaacagagagtttaaggccaaatattcccaacagatggca 1409
1393 AGAAATGAGAAAAAGTTGTTGTGAACAGAGAAGTTAAGGCCAAATATCCCAACAGATGGCA 1452
1410 gagctgtgagcccttgagagtgatggcccaaaatattatgagagaatgttggatgcgaatgg 1469
1453 GAGCTGTGAAGCCCTTGAGAGTAAATGCTTAAATATGAGAGAAATGTTGGTATGCCAATGG 1512

Db 390 tggcctcgtgctgtggagctggcagctgtcattgctggtccagctgtctctcgtcat 449
Qy 433 TGGCCTTGGTCTCTGTGGAACCTGGCAGCTGTCATTGCTGGACCGAGTGTCTTCTGTCAT 492
Db 450 tgcacttatgtgtgcttatctatctgccaataaacgcactgtcattcaccaccgctgccc 509
Qy 493 CTCACATCATGTTGATGGTCTATATCTGCCACAACCGCACTGTCTTACCATCCAGTGCC 552
Db 510 aaatgaagagagatccctcactagatcgccctttcatttcagagggcaccaccttaaaaga 569
Qy 553 AAATGAAGAGAGACCTTCTATTAGATCGCCCTTTTATTTCAGAGGGTACTACGTTGAAGA 612
Db 570 ttttaattatgatgacacaacatcagggtctggtatcaggtttaccactgcttcttcaag 629
Qy 613 CTTAAITTTATGATATGACAACGTGAGTCTGGCTCAGTTTACCATTGCTTGTTCAGAG 672
Db 630 aacaattgcaggaccattgtgtctacaagaagcatcggaagagtcggttttgagagagt 689
Qy 673 AACAAITGCGAGAATCTATTGCTTACAAGAAAGCATTTGGCAAAGTTCGATTTGGAGAAGT 732
Db 690 ttggcgaggcaaatggcggggagagaagtgcgcgtgaagatatctctctcttagagaaga 749
Qy 733 TTGGAGAGGAAAGTGGCGGGGAGAGAAGTTGCTGTGTAAGATATTTCTCTCTAGAGAAGA 792
Db 750 acgttcattggttcgagagagcagagatttatcagactgtaattgttacgccaataaatat 809
Qy 793 ACGTTCGTGTTCCGTGAGGAGAGATTTATCAAACTGTAATGTTACGTCATGAAAACAT 852
Db 810 cctgggggtttatagcagcagacaacaagaacatggtacatggtcagctcagctgtggttgg 869
Qy 853 CCTGGGATTTATAGCAGCAGACAATAAGACAATGGTACTTGGACTCAGCTCTGTTGGT 912
Db 870 gtgcgattatcatgagcagtggtgctccttttcgatttacttgatgaatagatacactgttactgt 929
Qy 913 GTCAGATTTATCATGAGCATGGATCCCTTTTGTATTACTTTAAACAGATACAGTTACTGT 972
Db 930 ggaagaaatgatcaaatcgctcgtccagggcaagtggtcttgcccatcttcacatgga 989
Qy 973 GGAAGGAATCATAAACTTGTCTGTCTCCAGCGGAGGGTCTTGCCCATCTTCCATGGA 1032
Db 990 gattgtgtgaccagaagaaaccagctattgcccataagagattggaatacaagaatat 1049
Qy 1033 GATTGTGTTACCAAGAAAGCCAGCCATTTGCTCATAGATTTGAAATCAAGAAATAT 1092
Db 1050 cttggtggaagaaaaatggaacctgtgtattgagatttgggaactgtgtgtgagacatga 1109
Qy 1093 CTTGGTAAAGAAAGAAATGGAACCTGCTGTATTGACAGCTTAGGAGTGGCAGATGA 1152
Db 1110 ttctgcccagatacaattgtatattgctccaaaccacagagtaggcaataaaggtatat 1169
Qy 1153 TTCAGCCACAGATACCATTTGATTTGCTCCAAACCACAGAGTGGGAACAAAAGGTACAT 1212
Db 1170 ggccctggaagttctatagatccataaatgaaacattttgaatccttcaacgtgc 1229
Qy 1213 GGGCCCTGGAAGTTCTCGATGATTCCTCAATAATATGAACAATTTTGAATCTTCAACGTGC 1272
Db 1230 tgacatctatgcaatggccttagtattctgggaaatcgctcagcgtgttccatggcgg 1289
Qy 1273 TGACATCTATGCAATGGCTTAGTATTCTGGGAAATTTGCTCGACGATGTTCCATTGGTGG 1332
Db 1290 aatccacgaagactaccagttgccttactatgatcttctgtaccttctgtatccatcggtga 1349
Qy 1333 AATTCAATGAAGATTACCAACTGCCCTTATTATGATCTTGTACTTCTGACCCCAACAGTTGA 1392
Db 1350 agaaatgagaaaaagtagttgtgaaacagagagtttaaggccaaatattcccaacagatggca 1409
Qy 1393 AGAAATGAGAAAAAGTTGTTGTGAACAGAGAAGTTAAGGCCAAATATCCCAACAGATGGCA 1452
Db 1410 gagctgtgagcccttgagagtgatggcccaaaatattatgagagaatgttggatgcgaatgg 1469
Qy 1453 GAGCTGTGAAGCCCTTGAGAGTAAATGCTTAAATATGAGAGAAATGTTGGTATGCCAATGG 1512

cds.
L26110
g416397
serine/threonine kinase receptor.
Rattus norvegicus (strain Sprague-Dawley) cDNA to mRNA.
Rattus norvegicus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Rattus.
1 (bases 1 to 1545)
He, W.W., Gustafson, M.L., Hirobe, S. and Donahoe, P.K.
Developmental expression of four novel serine/threonine kinase
receptors homologous to the activin/transforming growth factor-beta
type II receptor family
Dev. Dyn. 196 (2), 133-142 (1993)
93372378
2 (bases 1 to 1545)
Bassing, C.H., Yingling, J.M., Howe, D.J., Wang, T., He, W.W.,
Gustafson, M.L., Shah, P., Donahoe, P.K. and Wang, X.F.
A transforming growth factor beta type I receptor that signals to
activate gene expression
Science 263 (5143), 87-89 (1994)
94098329
Location/Qualifiers
1..1545
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/dev_stage="14.5-15 day fetus"
/tissue_type="urogenital ridge"
/clone="R4"
40..1545
/note="serine/threonine kinase receptor; TGF-beta type I"
/codon_start=1
/product="transforming growth factor beta type I receptor"
/db_xref="PID:g1113130"
/translation="MEASAAALRCLLIIVLVAATLLPGAKALQCFCHLCTKDNFTC
ETDGLCFVSTETTDKVIHNSMCIAEIDLIPDRPFVCAPSSKTGAVTYCCNODHONK
IELPTGTPSEKOSAGLGPVELAAVAGVCFVCIALLMVIYICHRVTVIHRVPNEE
DPSLRPFISGTTLDKLLIYDMTSGSGSLPLLQVRIARTIIVLQESIGKGRFGEVW
RGKRGEEVAVKIFSSREERSWFREAEIYQTVMLRHNILGFIADNDKNGTWTQLWL
VSDYHEHGSFLDYLNRYTVTVGEMIKLALSTASGLAHLHMEIVGTQGPALIAHRDLKS
KNILVKNGTCCITADGLAVELASATDIDIAPNRVGTRKRYMAPEVLDDSDINMKHFE
SFKRADIYAMGLVFEWETARRCSIGIHEDYQLPYDLVPSDPSVEEMRKVVCQKLRP
NIPNRQSCALVMKIMRCWYANGAARLTALRIKTLISQLSQOEGIKM"
BASE COUNT 435 a 335 c 380 g 395 t
ORIGIN
Seq Match 47.7%; Score 1102; DB 87; Length 1545;
Local Similarity 88.9%; Pred. No. 0.00e+00;
Matches 1294; Conservative 0; Mismatches 156; Indels 6; Gaps 5;
Db 90 ggtggcggcgagcgtgtcccgggggcgaaggcattacagttgttctgccacctctg 149
Qy 139 GCGCGCGGGCGCGCTGCTCCCGGGGCGAGCGGCTTACAGTGTTCGCGCACCTCTG 198
Db 150 tacaaggacaaatttactgtgagacagatggtctctgtctgtctcagtcacagagac 209
Qy 199 TACAAAAGACAATTTACTTGTGTGACAGATGGCTCTGCTTGTCTGTGTCACAGAGAC 258
Db 210 cacagacaaagtatacacaaatagcatgtgtatagctgaaatcgacctaatcccccgaga 269
Qy 259 CACAGACAAAGTTATACACAACAGCATGTGTATAGCTGAAATTCACATTAATTCCTCGAGA 318
Db 270 caggccatttggcaccatcttcaaaaacagggcgagtgactgtattgtcgaatca 329
Qy 319 TAGGCCGTTGTATGTGACACCTCTTCAAAAACCTGGGTCTGTGAC-TACAACAT--ATT- 374
Db 330 ggatcactgcaataaataagaactccccactacagacacctttttcagaaaaagcagtcagc 389
Qy 375 GCTGCAAT-CAGGACCATTCGAATAAATAAGA-ACITTCCAACTACTGTAAAGTCATCACC 432

Db 1470 agcagctaggctgacagctttgcgaattaaaaaacattgcacagctcagcgaacagga 1529
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1513 AGCAGTAGGCTTACAGCATTCGGATTGAAGAAACATTATCGCAACTCAGTCAACAGGA 1572
Db 1530 aggcatacaaatgtaa 1545
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1573 AGGCATCAAAATGTAA 1588

RESULT 9
LOCUS CHKRPK2 2186 bp mRNA VRT 09-DEC-1993
DEFINITION Chicken RPK-2 mRNA for receptor protein kinase, complete cds.
ACCESSION D14460
NID g285699
KEYWORDS TGF-beta receptor-related; receptor protein kinase;
serine/threonine kinase; transmembrane protein.
SOURCE Gallus gallus (library: lambda gt10) stage 24-26 (Hamburger &
Hamilton) cDNA to mRNA, clones S5 and S7.
ORGANISM Gallus gallus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Archosauria; Aves; Neognathae; Galliformes;
Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 2186)
Nohno,T., Sumitomo,S., Ishikawa,T., Ando,C., Nishida,S., Noji,S.
and Saito,T.
TITLE Nucleotide sequence of a cDNA encoding the chicken receptor protein
kinase of the TGF-beta receptor family
JOURNAL DNA Seq. 3 (6), 393-396 (1993)
MEDLINE 94033626

Query Match 36.1%; Score 832; DB 49; Length 2186;
Best Local Similarity 82.1%; Pred. No. 6.00e+00;
Matches 1181; Conservative 0; Mismatches 240; Indels 18; Gaps 7;
RESULT 13
LOCUS HSALK4A 2333 bp RNA PRI 29-SEP-1993
DEFINITION Homo sapiens ALK-4 mRNA, complete CDS.
ACCESSION Z22536
NID G402188
KEYWORDS ALK-4 gene; cell surface receptor; serine threonine kinase.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2333)
ten Dijke,P.P.
AUTHORS Direct Submission
TITLE Submitted (06-APR-1993) Peter P ten Dijke, Ludwig Institute for
Cancer Research, Uppsala, branch, Biomedical Center, Husargatan 3,
Uppsala, S-751 24, Sweden
REFERENCE 2 (bases 1 to 2333)
ten Dijke,P., Ichijo,H., Franzen,P., Schulz,P., Saras,J.,
Toyoshima,H., Heldin,C.H. and Miyazono,K.
AUTHORS Activin receptor-like kinases: a novel subclass of cell-surface
TITLE Activin receptor-like kinases: a novel subclass of cell-surface
receptors with predicted serine/threonine kinase activity
JOURNAL Oncogene 8 (10), 2879-2887 (1993)
MEDLINE 93390967

Query Match 20.8%; Score 481; DB 70; Length 2333;
Best Local Similarity 74.8%; Pred. No. 0.00e+00;
Matches 725; Conservative 0; Mismatches 244; Indels 0; Gaps 0;
MPerch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu Jun 26 04:43:27 1997; MasPar time 220.72 Seconds
Tabular output not generated. 967.382 Million cell updates/sec
Title: >US-08-436-265-9
Description: (1-2308) from US08436265.seq
Perfect Score: 2308

N.A. Sequence: 1 GCGAGGCGAGGTTTGCTGG.....TGTAAACCTATAGTGT 2308
Comp: CCGCTCCGCTCCAACGACC.....ACAATTTGGATATACAAA
Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 121476 seqs, 46255616 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: n-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
Statistics: Mean 9.949; Variance 6.392; scale 1.557
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES
Result No. Score Match Length DB ID Description Pred. No.
1 2280 98.8 2308 11 Q66638 Human Activin recepto 0.00e+00
2 1163 50.4 1794 14 Q83534 Sequence encoding ser 0.00e+00
3 1102 47.7 1506 22 T36068 Mullerian inhibiting 0.00e+00
4 1102 47.7 1506 8 Q49766 Misr4. 0.00e+00
5 481 20.8 2333 11 Q66637 Human Activin recepto 2.37e-290
6 471 20.4 1518 8 Q49764 Misr2A/misr2B. 1.01e-283
7 471 20.4 2160 11 Q66641 Mouse Activin recepto 1.01e-282
8 467 20.2 1647 14 Q83533 Sequence encoding ser 4.50e-281
9 462 20.0 1506 22 T36070 Mullerian inhibiting 9.23e-278
10 445 19.3 1482 20 T26994 Serine threonine kina 1.67e-266
ALIGNMENTS
RESULT 1
ID Q66638 standard; cDNA; 2308 BP.
AC Q66638;
DT 20-JAN-1995 (first entry)
DE Human Activin receptor-like kinase 5 (hALK-5) cDNA.
KW serine threonine kinases; activin receptors; Act-R; superfamily;
KW transforming growth factor; TGF; diagnostics; detection; therapy;
KW rheumatoid arthritis; glomerular nephritis; fibrosis; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT 5'UTR 1..76
FT /*tag= a
FT /note= "contains an in-frame stop codon at
FT nucleotides (-54)-(-52)"
FT CDS 77..1588
FT /*tag= b
FT /product= activin receptor-like kinase 5
FT 3'UTR 1589..2308
FT /*tag= c
FT /note= "3'UTR is a total of 3.7kb and was not
FT completely sequenced"
PN W09411502-A.
PD 26-MAY-1994.
PF 17-NOV-1993; G02367.
PR 17-NOV-1992; GB-024057.
PR 08-MAR-1993; GB-004677.
PR 08-MAR-1993; GB-004680.
PR 28-MAY-1993; GB-011047.

PT 02-JUL-1993; GB-013763.
PT 03-AUG-1993; GB-016099.
PT 15-OCT-1993; GB-021344.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Dijke P, Franzen P, Heidin C, Miyazono K, Yamashita H;
DR WPI; 94-183503/22.

RESULT 2
ID Q83534 standard; DNA; 1794 BP.
AC Q83534;
DT 28-SEP-1995 (first entry)
DE Sequence encoding serine/threonine kinase receptor W120.
KW Bone morphogenic protein; receptor; serine/threonine kinase; BMP;
KW bone; cartilage; injury; treatment; inhibition; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 83..1594
FT /*tag= a
FT /product= Serine/threonine kinase receptor.
PN W09507982-A.
PD 23-MAR-1995.
PF 07-SEP-1994; U10080.
PF 17-SEP-1993; US-123934.
PF (GEM) GENETICS INST INC.
PI Celeste AJ, Thies RS, Wozney JM, Yamaji N;
DR WPI; 95-131350/17.
DR P-PSDB; R70241.
PT Truncated BMP and serine/threonine kinase receptor proteins -
PT used to inhibit the effects of BMP-2 and/or BMP-4.
PS Claim 3; Page 64-66; 83pp; English.
CC Truncated bone morphogenic protein (BMP) receptors and
CC serine/threonine kinase receptors may be used in compositions to
CC inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated
CC receptors pref. comprise the ligand binding domain, but not the
CC serine/threonine kinase and transmembrane domains. The truncated
CC proteins are soluble and will be excreted into supernatant by
CC recombinant mammalian cells expressing them. Such cells can be
CC delivered in a medium or matrix which partially impedes their
CC mobility, thereby localising the cells to a site of bone or
CC cartilage injury.
SQ Sequence 1794 BP; 488 A; 390 C; 454 G; 462 T;

Query Match 50.4%; Score 1163; DB 14; Length 1794;
Best Local Similarity 89.0%; Pred. No. 0.00e+00;
Matches 1481; Conservative 0; Mismatches 156; Indels 27; Gaps 11;

PT 02-JUL-1993; GB-013763.
PT 03-AUG-1993; GB-016099.
PT 15-OCT-1993; GB-021344.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Dijke P, Franzen P, Heidin C, Miyazono K, Yamashita H;
DR WPI; 94-183503/22.

RESULT 3
ID Q83608 standard; cDNA; 1506 BP.
AC Q83608;
DT 30-OCT-1996 (first entry)
DE Mullerian inhibiting substance receptor coding sequence misr4.
KW Mullerian inhibiting substance receptor; MISR; TGF-beta receptor;
KW transforming growth factor beta type I receptor; gene therapy;
KW wound healing; tumour treatment; rat inhibin; ds.
OS Rattus sp.
FH Key Location/Qualifiers
FT CDS 1..1506
FT /*tag= a
FT /product= MISR4
PN US5538892-A.
PD 23-JUL-1996.
PF 18-MAR-1992; 853396.
PR 18-MAR-1992; US-853396.
PR 11-MAR-1993; US-029673.
PR 04-NOV-1993; US-149105.
PA (GEM) GEN HOSPITAL CORP.
PA (UYDU-) UNIV DUKE.
PI Donahoe PK, Gustafson M, He W, Wang X;
DR WPI; 96-353830/35.
DR P-PSDB; W03758.

Query Match 50.4%; Score 1163; DB 14; Length 1794;
Best Local Similarity 89.0%; Pred. No. 0.00e+00;
Matches 1481; Conservative 0; Mismatches 156; Indels 27; Gaps 11;

PT 02-JUL-1993; GB-013763.
PT 03-AUG-1993; GB-016099.
PT 15-OCT-1993; GB-021344.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Dijke P, Franzen P, Heidin C, Miyazono K, Yamashita H;
DR WPI; 94-183503/22.

RESULT 4
ID Q49766 standard; cDNA; 1506 BP.
AC Q49766;
DT 20-APR-1994 (first entry)
DE Misr4.
KW MIS; Mullerian Inhibitory Substance; receptor;
KW transforming growth factor; inhibin; BMP;
KW membrane serine/threonine kinase receptor;
KW bone morphogenesis protein; ss.
OS Rattus rattus.
PN W09319177-A.
PD 30-SEP-1993.
PF 15-MAR-1993; U02387.
PR 18-MAR-1992; US-853396.
PR 11-MAR-1993; US-029673.
PA (GEM) GEN HOSPITAL CORP.
PI Donahoe PK, Gustafson M, He WW;
DR WPI; 93-320743/40.
DR P-PSDB; R41923.
PT New receptors of the transforming growth factor-beta receptor
PT family - comprising Mullerian Inhibitory Substance Receptors and
PT inhibin receptors
PS Claim 53; Fig 4; 59pp; English.
CC Misr1 (Q49763) is believed to encode an isoform of the rat
CC MIS receptor. Misr2A/misr2B (Q49764), misr3 (Q49765) and misr4
CC (Q49766) are believed to encode monomeric isoforms of the rat
CC inhibin receptor and/or BMP receptor.
SQ Sequence 1506 BP; 428 A; 321 C; 363 G; 394 T;

Query Match 47.7%; Score 1102; DB 8; Length 1506;
Best Local Similarity 88.9%; Pred. No. 0.00e+00;
Matches 1294; Conservative 0; Mismatches 156; Indels 6; Gaps 5;

MPsrch_nm n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu Jun 26 04:47:38 1997; MasPar time 1458.40 Seconds
1014.493 Million cell updates/sec
Tabular output not generated.
Title: >US-08-436-265-9
Description: (1-2308) from US08436265.seq
Perfect Score: 2308
N.A. Sequence: 1 GGCGAGGCGAGGTTTGCTGG.....TGTTAAACCTATAGTGT 2308
Comp: CCGCTCGCTCCAAACGACC.....ACAATTGGATATACAAA

Nmatch STD : Dbase 0; Query 0
Searched: 887282 seqs, 320523884 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS
Result No. Score Match Length DB ID Description Pred. No.

No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	720	31.2	720	196	G06514	Human STS WI-7314.	0.00e+00
2	332	14.4	426	8	AA047142	zk74e04.r1 Soares pre	0.00e+00
3	332	14.4	426	230	HS47142	zk74e04.r1 Soares pre	0.00e+00
4	132	5.7	739	10	AA053838	zf53c07.r1 Soares ret	3.47e-210
5	132	5.7	739	231	HS43838	zf53c07.r1 Soares ret	3.47e-210
6	114	4.9	515	43	C17679	Human placenta cDNA 5	4.04e-172
7	114	4.9	515	239	HSC6799	Human placenta cDNA 5	4.04e-172
8	96	4.2	404	165	W39552	zc18g04.r1 Soares par	9.48e-135
9	92	4.0	631	168	W48139	mc85f09.r1 Soares mou	1.45e-126
10	87	3.8	471	164	W34981	mc33h08.r1 Soares mou	2.08e-116

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu Jun 26 05:12:37 1997; MasPar time 86.86 Seconds
Tabular output; not generated.

Title: >US-08-436-265-9
Description: (1-2308) from US08436265.seq
Perfect Score: 2308
N.A. Sequence: 1 GCGAGGCGAGGTTGCTGG.....TGTTAAACCTATAGTGT 2308
Comp: CCGCTCGCTCCAAACGACC.....ACAATTTGGATATCACAAA

Scoring table: TABLE default Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 60653 seqs, 16071407 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1:51 2:52 3:53 4:54 5:55 6:56 7:PCT90 8:PCT91 9:PCT92
10:PCT93 11:PCT94 12:PCT95 13:PCT96
Statistics: Mean 9.385; Variance 5.413; scale 1.734

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	1163	50.4	1794	11	PCT-US94-1	Sequence 9, Applicatio	0.00e+00
2	1102	47.7	1506	5	US-08-149-	Sequence 4, Applicatio	0.00e+00
3	1102	47.7	1506	5	US-08-317-	Sequence 4, Applicatio	0.00e+00
4	467	20.2	1647	11	PCT-US94-1	Sequence 7, Applicatio	0.00e+00
5	462	20.0	1506	5	US-08-149-	Sequence 2, Applicatio	0.00e+00
6	462	20.0	1506	5	US-08-317-	Sequence 2, Applicatio	0.00e+00
7	445	19.3	1482	6	US-08-341-	Sequence 1, Applicatio	4.51e-299
8	262	11.4	2076	11	PCT-US94-1	Sequence 3, Applicatio	8.90e-165
9	261	11.3	2932	12	PCT-US95-0	Sequence 5, Applicatio	4.75e-164

Database: a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19
Statistics: Mean 35.793; Variance 157.139; scale 0.228

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
ID PCT-US94-10080-9 STANDARD; DNA; UNC; 1794 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 9, Application PC/TUS9410080.
CC Sequence 9, Application PC/TUS9410080
CC GENERAL INFORMATION:
CC APPLICANT: GENETICS INSTITUTE, INC.
CC TITLE OF INVENTION: RECEPTOR PROTEINS
CC NUMBER OF SEQUENCES: 19
CC CORRESPONDENCE ADDRESS:
Query; Match 50.4%; Score 1163; DB 11; Length 1794;
East Local Similarity 89.0%; Pred. No. 0.00e+00;
Matches 1481; Conservative 0; Mismatches 156; Indels 27; Gaps 11;
MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Jun 24 17:58:06 1997; MasPar time 10.36 Seconds
Tabular output not generated.

Title: >US-08-436-265-10
Description: (1-503) from US08436265.pap
Perfect Score: 3687
Sequence: 1 MEAAVAAPRRLULLVIAA.....TALRIKKTLQSQQEGIKM 503

Scoring table: PAM 150 Gap 11
Searched: 92623 seqs, 10896596 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19
Statistics: Mean 35.793; Variance 157.139; scale 0.228

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	3657	99.2	503	10	R55370	Human Activin recepto	0.00e+00
2	3493	94.7	503	13	R70241	Serine/threonine kina	0.00e+00
3	3454	93.7	501	18	W03758	Mullerian inhibiting	0.00e+00
4	3454	93.7	501	8	R41923	MISR4.	0.00e+00
5	2517	68.3	505	13	R70240	Serine/threonine kina	7.49e-229
6	2517	68.3	505	10	R55373	Mouse Activin recepto	7.49e-229
7	2516	68.2	505	8	R41921	MISR2A/MISR2B.	9.38e-229
8	2515	68.2	505	10	R55369	Human Activin recepto	1.17e-228
9	2481	67.3	501	18	W03760	Mullerian inhibiting	2.46e-225
10	2384	64.7	493	17	R95562	Serine threonine kina	7.30e-216

ALIGNMENTS
RESULT 1
ID R55370 standard; Protein; 503 AA.
AC R55370;
DT 20-JAN-1995 (first entry)
DE Human Activin receptor-like kinase 5 (hALK-5).

serine threonine kinases; activin receptors; Act-R; superfamily;
 KW transforming growth factor; TGF; diagnostics; detection; therapy;
 KW rheumatoid arthritis; glomerular nephritis; fibrosis.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /label= putative signal peptide
 FT Protein 25..503
 FT /label= activin receptor-like kinase 5
 FT /note= "mature protein"
 PN W09411502-A.
 PD 26-MAY-1994.
 PF 17-NOV-1993; G02367.
 PR 17-NOV-1992; GB-024057.
 PR 17-NOV-1993; GB-004677.
 PR 17-MAR-1993; GB-004680.
 PR 28-MAY-1993; GB-011047.
 PR 02-JUL-1993; GB-013763.
 PR 03-AUG-1993; GB-016099.
 PR 15-OCT-1993; GB-021344.
 PA (LUDW-) LUDWIG INST CANCER RES.
 Query Match 99.2%; Score 3657; DB 10; Length 503;
 Best Local Similarity 99.4%; Pred. No. 0.00e+00;
 Matches 500; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 MEAAVAAPRLLLVLAASAAAALPGATAIGCFNHTKDNFTCTDGLCFVSVE 60
 1 MEAAVAAPRLLLVLAASAAAALPGATALQCFCHLCTKDNFTCTDGLCFVSVE 60
 61 TDKVHNSMCIAEIDLIPDRPFVCAVSSKTSVTTTCNQHCKNIELPTTVKSSPG 120
 61 TDKVHNSMCIAEIDLIPDRPFVCAVSSKTSVTTTCNQHCKNIELPTTVKSSPG 120
 121 LGPVELAAVAGPVCVCSISLMVYICHNRTVIHHRVNEEDPSLDRPFISEGTTLKD 180
 121 LGPVELAAVAGPVCVCSISLMVYICHNRTVIHHRVNEEDPSLDRPFISEGTTLKD 180
 181 IYDNTSSGSLPLLVQRTIARTIVLQESIGKRGFGEVWGRGEEVAVNIFSSREER 240
 181 IYDNTSSGSLPLLVQRTIARTIVLQESIGKRGFGEVWGRGEEVAVNIFSSREER 240
 241 SWFREAEIYQTVMLRHNILGFIADNKNKNGTWTQLWLSVSDYHEHGSFLDYLNRYT 300
 241 SWFREAEIYQTVMLRHNILGFIADNKNKNGTWTQLWLSVSDYHEHGSFLDYLNRYT 300
 301 GMIKLALSTASGLAHLHMEIVGTQGPAPAHRLDKSKNILVKKNGTCTCIADIGLAVRHDS 360
 301 GMIKLALSTASGLAHLHMEIVGTQGPAPAHRLDKSKNILVKKNGTCTCIADIGLAVRHDS 360
 361 ATDTIDIAPNHRVGTGRYMAPEVLDSDSINMKHFSFKRADIYANGLVFWEIARRCSIGGI 420
 361 ATDTIDIAPNHRVGTGRYMAPEVLDSDSINMKHFSFKRADIYANGLVFWEIARRCSIGGI 420
 421 HEDYQLPYDYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCALRVMAKIMRECWWANGA 480
 421 HEDYQLPYDYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCALRVMAKIMRECWWANGA 480
 481 ARLTALRIKKTLSQLSQEGGIKM 503
 481 ARLTALRIKKTLSQLSQEGGIKM 503

RESULT 2

ID R70241 standard; Protein; 503 AA.
 AC R70241;
 DT 28-SEP-1995 (first entry)
 DE Serine/threonine kinase receptor W120.
 KW Bone morphogenic protein; receptor; serine/threonine kinase; BMP;
 KW bone; cartilage; injury; treatment; inhibition.
 OS Mus musculus.

PN W09507982-A.
 PD 23-MAR-1995.
 PF 07-SEP-1994; U10080.
 PR 17-SEP-1993; US-123934.
 PA (GEMY) GENETICS INST INC.
 PI Celeste AJ, Thies RS, Wozney JM, Yamaji N;
 DR WPI; 95-131350/17.
 DR N-PSDB; Q83534.
 PT Truncated BMP and serine/threonine kinase receptor proteins -
 PT used to inhibit the effects of BMP-2 and/or BMP-4.
 PS Claim 26; Page 67-68; 83pp; English.
 CC Truncated bone morphogenic protein (BMP) receptors and
 CC serine/threonine kinase receptors may be used in compositions to
 CC inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated
 CC receptors pref. comprise the ligand binding domains. The truncated
 CC serine/threonine kinase and transmembrane domains. The truncated
 CC proteins are soluble and will be excreted into supernatant by
 CC recombinant mammalian cells expressing them. Such cells can be
 CC delivered in a medium or matrix which partially impedes their
 CC mobility, thereby localising the cells to a site of bone or
 CC cartilage injury.
 SQ Sequence 503 AA;

Query Match 94.7%; Score 3493; DB 13; Length 503;
 Best Local Similarity 95.7%; Pred. No. 0.00e+00;
 Matches 485; Conservative 5; Mismatches 9; Indels 8; Gaps 3;
 1 MEAAVAAPRLLLVLAASAAAALPGATALQCFCHLCTKDNFTCTDGLCFVSVE 60
 1 MEAAVAAPRLLLVLAASAAAALPGATALQCFCHLCTKDNFTCTDGLCFVSVE 60
 57 TDKVHNSMCIAEIDLIPDRPFVCAVSSKTSVTTTCNQHCKNIELPTTVKSSPG 116
 57 TDKVHNSMCIAEIDLIPDRPFVCAVSSKTSVTTTCNQHCKNIELPTTVKSSPG 116
 61 TDKVHNSMCIAEIDLIPDRPFVCAVSSKTSVTTTCNQHCKNIELPTTVKSSPG 116
 61 TDKVHNSMCIAEIDLIPDRPFVCAVSSKTSVTTTCNQHCKNIELPTTVKSSPG 116
 117 LGPVELAAVAGPVCVCSISLMVYICHNRTVIHHRVNEEDPSLDRPFISEGTT 176
 117 LGPVELAAVAGPVCVCSISLMVYICHNRTVIHHRVNEEDPSLDRPFISEGTT 176
 177 IYDNTSSGSLPLLVQRTIARTIVLQESIGKRGFGEVWGRGEEVAVNIFSS 236
 177 IYDNTSSGSLPLLVQRTIARTIVLQESIGKRGFGEVWGRGEEVAVNIFSS 236
 237 SWFREAEIYQTVMLRHNILGFIADNKNKNGTWTQLWLSVSDYHEHGSFLDYLNRYT 296
 237 SWFREAEIYQTVMLRHNILGFIADNKNKNGTWTQLWLSVSDYHEHGSFLDYLNRYT 296
 297 VTVEGMIKLALSTASGLAHLHMEIVGTQGPAPAHRLDKSKNILVKKNGTCTCIADIGLAV 356
 297 VTVEGMIKLALSTASGLAHLHMEIVGTQGPAPAHRLDKSKNILVKKNGTCTCIADIGLAV 356
 357 RHDSDATDTIDIAPNHRVGTGRYMAPEVLDSDSINMKHFSFKRADIYANGLVFWEIARRCS 416
 357 RHDSDATDTIDIAPNHRVGTGRYMAPEVLDSDSINMKHFSFKRADIYANGLVFWEIARRCS 416
 417 IGGIHEDYQLPYDYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCALRVMAKIMRECWW 476
 417 IGGIHEDYQLPYDYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCALRVMAKIMRECWW 476
 477 ANGAARLTALRIKKTLSQLSQEGGIKM 503
 477 ANGAARLTALRIKKTLSQLSQEGGIKM 503

RESULT 3

ID W03758 standard; Protein; 501 AA.
 AC W03758;
 DT 30-OCT-1996 (first entry)
 DE Mullerian inhibiting substance receptor MISR4.
 KW Mullerian inhibiting substance receptor; MISR; TGF-beta receptor;
 KW transforming growth factor beta type I receptor; gene therapy;


```

KW Bone morphogenic protein; receptor; serine/threonine kinase; BMP;
KW bone; cartilage; injury; treatment; inhibition.
OS Mus musculus.
PN WO9507982-A.
PD 23-MAR-1995.
PF 07-SEP-1994; U10080.
PR 17-SEP-1993; US-123934.
PA (GEMY ) GENETICS INST INC.
PI Celeste AJ, Thies RS, Wozney JM, Yamaji N;
DR WPI; 95-131350/17.
DR N-PSDB; Q83533.
PT Truncated BMP and serine/threonine kinase receptor proteins -
PT used to inhibit the effects of BMP-2 and/or BMP-4.
PS Claim 25; Page 63-64; 83pp; English.
PC Truncated bone morphogenetic protein (BMP) receptors and
CC serine/threonine kinase receptors were used in compositions to
CC inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated
CC serine/threonine kinase and transmembrane domains. The truncated
CC proteins are soluble and will be excreted into supernatant by
CC recombinant mammalian cells expressing them. Such cells can be
CC delivered in a medium or matrix which partially impedes their
CC mobility, thereby localising the cells to a site of bone or
CC cartilage injury.
SC Sequence 505 AA;

Query Match      68.3%; Score 2517; DB 13; Length 505;
Best Local Similarity 71.2%; Pred. No. 7,49e-229;
Matches 356; Conservative 62; Mismatches 65; Indels 17; Gaps 14;

RESULT          6
ID R55373 standard; Protein; 505 AA.
AC R55373;
DT 20-JAN-1995 (first entry)
DE Mouse Activin receptor-like kinase 4 (mALK-4).
KE serine threonine kinases; activin receptors; Act-R; superfamily;
KW transforming growth factor; TGF; diagnostics; detection; therapy;
KW rheumatoid arthritis; glomerular nephritis; fibrosis.
OS Mus musculus.
PN WO9411502-A.
PD 26-MAY-1994.
PF 17-NOV-1993; G02367.
PR 17-NOV-1992; GB-024057.
PR 08-MAR-1993; GB-004677.
PR 08-MAR-1993; GB-004680.
PR 28-MAY-1993; GB-011047.
PR 02-JUL-1993; GB-013763.
PR 03-AUG-1993; GB-016099.
PR 15-OCT-1993; GB-021344.

Query Match      68.3%; Score 2517; DB 10; Length 505;
Best Local Similarity 71.2%; Pred. No. 7,49e-229;
Matches 356; Conservative 62; Mismatches 65; Indels 17; Gaps 14;

Db    13 lvvllltagsggp-rgiqallcactscldtntctcdgacmvsfnl-dgvehhvrtci 70
QY   ||| :||::: | ||| | | | | | | | | | | | | | | | | | | | | |
       LLVLAAAAAAAALLPGATALQFCFLCXTKDNFTCVTDGLCFVSVTETTDKVHNN-SMCI 72

Db    71 pkvelvpagkpfycl-sse--dlrnthccyidfcnkidlrpsghlkpeahpsmgwpgvel 127
QY   :::||::| | | | | | | | | | | | | | | | | | | | | | | | | | |
       AEIDLIPRDPFVCAPSSKYGVSTTYTCNQDHCKNKLIEL--PTT-VK-SS-PGL-GPVEL 126

Db    128 vgiaggvfllfliiliivflvinylhyar-vyhnrqrldmedpscenc-lskdktlqdlvyd 185
QY   :::||vv| | | | | | | | | | | | | | | | | | | | | | | | | | |
       AAVTAGPYVC--FVICSLMLVMVYTCHNRVTIHRHPVNE--EDPSLDRPFI SEGTTLKDLYD 183

Db    186 lstsgsgslplfvrtartvltqlqeilgrfgevwrvgdwavkfisreerswf 245
QY   :::||::| | | | | | | | | | | | | | | | | | | | | | | | | | |
       MTTSGGSGSLPLLVQRTIARTIVQLVESIGKRFGFEVRWKGWRGEEVAVKIFSSREERSWF 243

Db    246 reaaiqtvtmlrhenilgfiaadknkdngwtqlwlvsdyhehgslfdynryvcvtieqm 305

```

244	QY	REAEITYQTVMLRHEHIIIGFIAADNKNXGNTWTQLWLVSDYHEHGSFDFYLNRYTVTVVEGMI	303
306	Db	klalasaasglahlhmeivgtgkpgkiahrdlksknllvknmgmaeiadlglavrhdaavtd	365
304	QY	KLALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILLVKNNGTCCIIADLGLAVRHDSATD	363
366	Db	tidiapnqrvtgkrymapevldetimkhfdfsckadiyalglvyveiarncnsggvhed	425
364	QY	TIDIAPNHRVGTKRYMAPEVLDDSNMKHFESFKRADIYANGLVFWEIARRCSIGIHED	423
426	Db	yqlpyvdlvpsdpsieemkrvvcdgklrpnvpnwqsyrealrvmgkmmrcwyangaarl	485
424	QY	YOLPYVLDVPSDPSVEEMKRVVCEQKLRPNIPNRWQSCALRVMAKIMRCWYANGAARL	483
496	Db	talrikktlsqlsvqgedvki	505
484	QY	TALRIKKTLSQLSQOEGIKM	503

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Parsed: Tue Jun 24 17:58:55 1997; MasPar time 18.25 Seconds
 MasPar output not generated. 785.825 Million cell updates/sec

```
>US-08-436-265-10
Description: (1-503) from US08436265.pep
Perfect Score: 3687
Sequence: 1 MEAAVAAPRRLLILVLA...TALRTKLTLSLQSQEIKM 503
```

Scoring cable: ; PAM 150
Gap 11

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

```
Database:
      pir50
      1:ann1 2:ann2 3:ann3 4:ann4 5:annn1 6:unann2 7:unann3
      8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
      13:unann9 14:unann10 15:unrev 16:unrev
```

Statistics: Mean 48.912; Variance 115.163; scale 0.425

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query		Length	DB	ID	Description	Pred. No.
		Match						
1	3687	100.0	503	13	A49432		activin receptor-like transforming growth	0.00e+00
2	3536	95.9	499	14	JC2062		transforming growth	0.00e+00
3	3493	94.7	503	14	JC2061		transforming growth	0.00e+00
4	3020	81.9	440	13	A56693		receptor protein kin	0.00e+00
5	2522	68.4	505	13	I38859		activin receptor Act	0.00e+00
6	2522	68.4	505	13	I37164		ALK-4 - human	0.00e+00
7	2516	68.2	505	14	I53417		type I serine-threon	0.00e+00
8	2204	59.8	476	13	I80182		activin type I recep	0.00e+00
9	2021	54.8	601	12	A55921		serine/threonine kin	0.00e+00
10	1893	51.3	487	13	I80183		activin type I recep	0.00e+00

RESULT	1
ENTRY	A49432
TITLE	activin receptor-like kinase 5 precursor - human
ALTERNATE_NAMES	TGFbeta type I receptor ALK-5
CONTAINS	protein kinase (EC 2.7.1.37)

SUMMARY	#length 503	#molecular-weight	56178	#checksum	22559		
Query Match	94.7%;	Score	3493;	DB 14;	Length 503;		
Best Local Similarity	95.7%;	Pred. No.	0.00e+00;				
Matches	485;	Conservative	5;	Mismatches	9; Indels 8; Gaps 3;		
Db	1	mea	aaagarrpqlilvlva	aaat---	llpgakalqcfchlctkdnftc	etdglcfvsvte	56
Qy	1	MEAAVAAPRPR	LLVLA	AAAAA	ALLPGATALQCFCHLCTKDNFTCTV	DTDGLCFVSVTE	60
Db	57	trdkvi	hmsciaeidli	prdrpfvcapssktgavttt	ycnqdhcnkieltptg	fsek	116
Qy	61	TTDKVIHNSMCIAE	IDLIPDRDRPFVCAPSSKTSVT	TTTTCYCNQDHCNKIE	LPTT---	V-K	116
Db	117	qsaglgp	velaaviagpvcfvcialm	lmyichnrtv	vihrvnp	eedpsldrpfisegt	176
Qy	117	SSPGLGPVELAA	VIAGPVCFCVCSLM	VMYICHNRTVI	HRVNP	EEDEPSLDRPFISEGTT	176

QY 304 KLAISTAGLAHLHMEIVGTQKPAIAHRDLKSNILVKNNGTCCIALDLGLAVRHDSATD 363

Db 301 tidianphrvgtkrymapelvlddsinnmkhfsfradiyamglvfwelarrcsigghied 360

QY 364 TIDIAPNHRVGTKRYMAPEVLDDSIINMKHFSFKRADIYAMGLVFWELARRCSIGGHIED 423

Db 361 yqlpydyldvpsdpsveemkvvcqglrpnibnrvgscealrvmakinrecwyangaarl 420

QY 424 YQLPYDYLDVPSDPSVEEMKVVCEQLRPNIENRWSCEALRVNAKINRECYANGAARL 483

Db 421 talrikktlsqslsggegikm 440

QY 484 TALRIKKTLSQSLSGGEGIKM 503

RESULT 3

ENTRY 138859 #type complete

TITLE activin receptor ActR-IB, type I - human

ALTERNATE_NAMES ALK-4 protein

ORGANISM #formal_name Homo sapiens #common_name man

DATE 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 12-Apr-1996

ACCESSIONS 138859; S37184

REFERENCE A56060

#authors Carcamo, J.; Weis, F.M.; Ventura, F.; Wieser, R.; Wtana, J.L.; Attisano, L.; Massague, J.

#journal Mol. Cell. Biol. (1994) 14:3810-3821

#title Type I receptors specify growth-inhibitory and transcriptional responses to transforming growth factor beta and activin.

#cross-references MIM:254839

#accession 138859

#status preliminary

#molecule_type mRNA

#residues 1-505 #label RES

#cross-references EMBL:U14722; NID:g555933; CDS_PID:g555934

REFERENCE S37181

#authors ten Dijke, P.P.; Ichijo, H.H.; Franzen, P.P.; Schulz, P.P.; Saras, J.J.; Toyoshima, H.H.; Heldin, C.C.; Miyazono, K.K.

#submission Submitted to the EMBL Data Library, April 1993

#description Activin receptor-like kinases, A novel subclass of cell surface receptors with predicted serine/threonine kinase activity.

#accession S37184

#status preliminary

#molecule_type mRNA

#residues 1-505 #label TEN

#cross-references EMBL:222536

CLASSIFICATION #superfamily protein kinase homology

FEATURE 205-501

SUMMARY #length 505 #molecular-weight 56806 #checksum 3363

Query Match 68.4%; Score 2522; DB 13; Length 505;

Best Local Similarity 70.7%; Pred. No. 0.00e+00;

Matches 353; Conser

RESULT 9

ENTRY #type complete

TITLE serine/threonine kinase Atr-1 - fruit fly (Drosophila melanogaster)

ORGANISM #formal_name Drosophila melanogaster

DATE 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 08-Dec-1995

ACCESSIONS A55921

REFERENCE A55921

#authors Wrana, J.L.; Tran, H.; Attisano, L.; Arora, K.; Childs, S.R.; Massague, J.; O'Connor, M.B.

#journal Mol. Cell. Biol. (1994) 14:944-950

#title Two distinct transmembrane serine/threonine kinases from Drosophila melanogaster form an activin receptor complex.

#accession A55921

#status preliminary

#molecule_type mRNA

#residues 1-601 #label WRA

#cross-references GB:U04692

CLASSIFICATION #superfamily protein kinase homology

FEATURE 301-597

SUMMARY #length 601 #molecular-weight 67219 #checksum 801

Query Match 54.8%; Score 2021; DB 12; Length 601;

Best Local Similarity 58.6%; Pred. No. 0.00e+00;

Matches 279; Conservative 77; Mismatches 111; Indels 9; Gaps 8;

RESULT 11

ENTRY A53444 #type complete

TITLE activin receptor-like kinase 6 precursor - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 19-May-1994 #sequence_revision 19-May-1994 #text_change 08-Dec-1995

ACCESSIONS A53444; S40159

REFERENCE A53444

#authors ten Dijke, P.; Yamashita, H.; Ichijo, H.; Franzen, P.; Laiho, M.; Miyazono, K.; Heldin, C.H.

#journal Science (1994) 264:101-104

#title Characterization of type I receptors for transforming growth factor-beta and activin.

#accession A53444

#status preliminary

#molecule_type mRNA

#residues 1-502 #label TEN

#cross-references GB:223143

REFERENCE S40158

#authors Miyazono, K.; Moren, A.; Grimsby, S.; Ichijo, H.; Heldin, C.; ten Dijke, P.

#submission Submitted to the EMBL Data Library, June 1993

#description ALK-3 and ALK-6: the closely related members in the serine/threonine kinase receptor family.

#accession S40159

#status preliminary

#molecule_type mRNA

#residues 1-502 #label MIY

#cross-references EMBL:223143

CLASSIFICATION #superfamily protein kinase homology

FEATURE 202-498

SUMMARY #length 502 #molecular-weight 56944 #checksum 5099

Query Match 48.6%; Score 1793; DB 14; Length 502;

Best Local Similarity 54.0%; Pred. No. 1.36e-287;

Matches 266; Conservative 84; Mismatches 124; Indels 19; Gaps 15;

Db 18 gestaptprpkilrckchhhpcdsdvnnicstdgycftmieedddsgmpvvtsgclg-le- 75

QY 22 AAAAAALLPGATALQCFCHL-CTKD--NFTCVTDGLCFVSVTET-TDKVIHNSMCIAEIDL 77

Db 76 -gsd-fqcrdtphqrrsieccternecnk-dlhptlpklkdrfdvdpnhkallis 131

QY 78 IPDRPFVCAVPSKSGTGVTTTYCCNQ-DHCNKTEL-PT--TVKSSPGL-GPVELAAV-IA 131

Db 132 vtvcsl-l-lvllilfcyfykrgearpysigleqdetypggeslrldlieqsgsgsg 189

QY 132 GPVCFVCSILMLMVIICHNRTVHH-RVNEEDPSLDRPFISEGTTKLDLYDMTTSGS 190

Db 190 sglpllvrtiaqigmvkgikgrygevmgkwgkvavkvftteeaswfrteiyq 249

QY 191 SGLPLLVQRTIARTIVLQESIGKGFGEVWRGKWRGEEVAVKIPSSREERSWFRAEIYQ 250

Db 250 tvlmrhenilgffiaadiktgtswtqlylitdyhengslgydksttdaksmklaysv 309

QY 251 TVMLRHEINILGFAANDKNGTWTQLMLVSDVHEHGLFDYLNRYTVTVGMIKLLALSTA 310
Db 310 sgllhlteifstgkpaiahrdlksnllvkngtcciadlglavkfisdnevdipppn 369
QY 311 SGLAHLHMEIVTQGRPAIAHRLDKSNILVKNGTCCIAADLGLAVRHSATDTIDAPN 370
Db 370 trvgtkrymppevldealnhrnfqsyimadmsyfglllweiarrrcvsggveeyqlpyhd 429
QY 371 HRVGTKRYMAPBEVLDSINMKHFEFRADIVAMGLVFWFIARCSIGSIHEDYQIPLYD 430
Db 430 lvpdpssvedmeivcmkklrpsfpnrwssdecltgmkgklmtcewagpnasrltalrvkk 489
QY 431 LVPDPSVEEMRKVCQEKLRPNIPNRWQSCALRVMAKIMRECWMYANGAARLTALRIKK 490
Db 490 Lxkmsesgdikl 502
QY 491 TLSQISQOEGIKM 503

Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Jun 24 18:00:22 1997; MasPar time 12.51 Seconds
852.767 Million cell updates/sec
Talar output not generated.

Description: >US-08-436-265-10
(1-503) from US08436265.pep
Perfect Score: 3687
Sequence: 1 MEAAVAAPRPLLILVLA...TALRIKTLSQLSQOEGIKM 503

Scoring table: PAM 150
Gap 11
Searched: 59021 seqs, 21210388 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11
Statistics: Mean 50.633; Variance 86.716; scale 0.584

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Match	Length	Pred. No.
1	3687	100.0	503	5
2	3454	93.7	501	5
3	2522	68.4	505	5
4	2516	68.2	505	5
5	1793	48.6	502	5
6	1792	48.6	502	5
7	1770	48.0	532	5
8	1762	47.8	532	5
9	1651	44.8	509	5
10	1646	44.6	509	5

ALIGNMENTS
RESULT 1
ID KIR4 HUMAN STANDARD; PRT; 503 AA.
AC P36897;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

DE SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4 PRECURSOR (EC 2.7.1.37)
DE (SKR4) (ACTIVIN RECEPTOR-LIKE KINASE 5) (ALK-5) (TGF-BETA TYPE I RECEPTOR).
DE OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE; 94061986.
RA FRANZEN P., TEN DIJKE P., ICHJO H., YAMASHITA H., SCHULZ P.,
RA HELDIN C.H., MIYAZONO K.;
RL CELL 75:681-692(1993).
CC -!- FUNCTION: TYPE I/TYPE II TGF-BETA RECEPTORS FORM AN HETEROMERIC
CC COMPLEX AFTER BINDING TGF-BETA AT THE CELL SURFACE AND ACT AS
CC SIGNAL TRANSDUCERS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: FOUND IN ALL TISSUES EXAMINED, MOST ABUNDANT
CC IN PLACENTA AND LEAST ABUNDANT IN BRAIN AND HEART.
CC -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
CC PROTEIN KINASES. STRONG, TO ACTIVIN RECEPTORS.
Query Match 100.0%; Score 3687; DB 5; Length 503;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 503; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
ID KIR4 RAT STANDARD; PRT; 501 AA.
AC P80204;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4 PRECURSOR (EC 2.7.1.37)
DE (SKR4) (TGF-BETA TYPE I RECEPTOR).
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=UROGENITAL RIDGE;
RX MEDLINE; 93372378.
RA HE W.-W., GUSTAFSON M., HIROBE S., DONAHOE P.;
RL DEV. DYN. 196:133-142(1993).
CC -!- FUNCTION: TYPE I/TYPE II TGF-BETA RECEPTORS FORM AN HETEROMERIC
CC COMPLEX AFTER BINDING TGF-BETA AT THE CELL SURFACE AND ACT AS
CC SIGNAL TRANSDUCERS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: UROGENITAL RIDGE, TESTIS, OVARY, BRAIN AND LUNGS.
CC -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
CC PROTEIN KINASES. STRONG, TO ACTIVIN RECEPTORS.

EMBL; L26110; G1113130; -
DR PROSITE; PS00107; PROTEIN KINASE ATP.
DR PROSITE; PS00108; PROTEIN KINASE ST.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM.
KW RECEPTOR; TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;
KW TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 501 SERINE/THREONINE KINASE RECEPTOR R4.
FT DOMAIN 23 123 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 124 146 POTENTIAL.
FT DOMAIN 147 501 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 203 493 PROTEIN KINASE.
FT NP_BIND 209 217 ATP (BY SIMILARITY).
FT BINDING 230 230 ATP (BY SIMILARITY).
FT ACT_SITE 331 331 BY SIMILARITY.
FT CARBOHYD 41 41 POTENTIAL.
SQ SEQUENCE 501 AA; 55999 MW; 67D99EAB CRC32;

Query Match 93.7%; Score 3454; DB 5; Length 501;
Best Local Similarity 95.3%; Pred. No. 0.00e+00;
Matches 483; Conservative 5; Mismatches 9; Indels 10; Gaps 4;

DR PROSITE; PS00108; PROTEIN KINASE ST.
KW PROSITE; PS50011; PROTEIN KINASE DOM.
DR RECEPTOR; TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;
KW TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 505 SERINE/THREONINE KINASE RECEPTOR R2.
FT DOMAIN 24 126 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 127 149 POTENTIAL.
FT DOMAIN 150 505 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 207 497 PROTEIN KINASE.
FT NP BIND 213 221 ATP (BY SIMILARITY).
FT BINDING 234 234 ATP (BY SIMILARITY).
FT ACT SITE 335 335 BY SIMILARITY.
FT CARBOHYD 43 43 POTENTIAL.
SQ SEQUENCE 505 AA; 56806 MW; 85564CP7 ARC32;
Query Match 68.4%; Score 2522; DB 5; Length 505;
Best Local Similarity 70.7%; Pred. No. 0.00e+00;
Matches 353; Conservative 62; Mismatches 69; Indels 15; Gaps 11;
Mfarch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Jun 24 18:01:25 1997; MasPar time 5.11 Seconds
358.162 Million cell updates/sec
Tabular output not generated.
Titre: >US-08-436-265-10
Description: (1-503) from US08436265.pep
Perfect Score: 3687
Sequence: 1 MEAAVAAPRPLLLVLA...TALRIKTLSQLSQEGIKM 503
Scoring table: PAM 150
Gap 11
Searched: 39797 seqs, 3636180 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-issued
1:51 2:52 3:53 4:54 5:55 6:56 7: PCT90 8: PCT91 9: PCT92
10: PCT93 11: PCT94 12: PCT95 13: PCT96
Statistics: Mean 33.610; Variance 164.611; scale 0.204
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES
Result No. Score Match Length DB ID Description Pred. No.
1 3493 94.7 503 11 PCT-US94-1 Sequence 10, Applicati 7.01e-292
2 3454 93.7 501 5 US-08-317- Sequence 17, Applicati 1.88e-288
3 3454 93.7 501 5 US-08-149- Sequence 17, Applicati 1.88e-288
4 2517 68.3 505 11 PCT-US94-1 Sequence 8, Applicatio 3.61e-206
5 2481 67.3 501 5 US-08-149- Sequence 15, Applicati 5.17e-203
6 2481 67.3 501 5 US-08-317- Sequence 15, Applicati 5.17e-203
7 2384 64.7 493 6 US-08-341- Sequence 2, Applicatio 1.63e-194
8 1793 48.6 502 12 PCT-US95-0 Sequence 8, Applicatio 7.87e-143
9 1785 48.4 502 11 PCT-US94-1 Sequence 4, Applicatio 3.93e-142
10 1769 48.0 532 11 PCT-US94-1 Sequence 2, Applicatio 9.77e-141
ALIGNMENTS
RESULT 1
ID PCT-US94-10080-10 STANDARD; PRT; 503 AA.
XX
AC xxxxxx
XX

DT 01-JAN-1900

Sequence 10, Application PC/TUS9410080.
Sequence 10, Application PC/TUS9410080
GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
Query Match 94.7%; Score 3493; DB 11; Length 503;
Best Local Similarity 95.7%; Pred. No. 7.01e-292;
Matches 485; Conservative 5; Mismatches 9; Indels 8; Gaps 3;

RESULT 2
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AC xxxxxx
DT 01-JAN-1900
DE
DE Sequence 17, Application US/08317847.

Sequence 17, Application US/08317847
Patent No. 5547854
GENERAL INFORMATION:
APPLICANT: Donahoe, Patricia K.
APPLICANT: Gustafson, Michael
APPLICANT: He, Wei W.
TITLE OF INVENTION: FOUR NOVEL RECEPTORS OF THE TGF-B
NUMBER OF SEQUENCES: 17
TITLE OF INVENTION: FAMILY
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,847
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,673
FILING DATE: March 11, 1993
APPLICATION NUMBER: 07/853,396
FILING DATE: March 18, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/127002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 501
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
SEQUENCE 501 AA; 55999 MW; 1252583 CN;

Query Match 93.7%; Score 3454; DB 5; Length 501;
Best Local Similarity 95.3%; Pred. No. 1.88e-288;

Matches 483; Conservative 5; Mismatches 9; Indels 10; Gaps 4;
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Db 57 TTDKVIHNSMCIAEIDLIPDRPFVCPAPSKTGAUT--YCCNQDHCKNIELPTTGPFSK 114
Qy 61 TTDKVIHNSMCIAEIDLIPDRPFVCPAPSKTGSVTTCYCCNQDHCKNIELPTT--V-K 116
Db 115 QSAGLGPVELAAVIAAGPVCFVCIALMLMVYICHNRTVIHHRVNEEDPSIDRPFISEGTT 174
Qy 117 SSPGLGEVELAAVIAAGPVCFVCIALMLMVYICHNRTVIHHRVNEEDPSIDRPFISEGTT 176
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Qy 297 VTVEGMKIALSTASGLAHLHMEIVGTQKPAIAHRDLKSNILVKNGTCCIAADIGLAV 356
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Db 415 IGGIHEDYQLPYDLPSPDPSVEEMKRVCEQKLRPNIPNRWQSCALRVMAKIMRECWY 474
Qy 417 IGGIHEDYQLPYDLPSPDPSVEEMKRVCEQKLRPNIPNRWQSCALRVMAKIMRECWY 476
Db 475 ANGAARLTALRIKKTLSQSQEGIKM 501
Qy 477 ANGAARLTALRIKKTLSQSQEGIKM 503

RESULT 3
ID US-08-149-105-17 STANDARD; PRT; 501 AA.
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AC xxxxxx
DT 01-JAN-1900
DE
DE Sequence 17, Application US/08149105.
CC
CC Sequence 17, Application US/08149105
CC Patent No. 5538892
RESULT 4
ID PCT-US94-10080-8 STANDARD; PRT; 505 AA.
XX
AC xxxxxx
DT 01-JAN-1900
DE
DE Sequence 8, Application PC/TUS9410080.
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CC Sequence 8, Application PC/TUS9410080
CC GENERAL INFORMATION:
CC APPLICANT: GENETICS INSTITUTE, INC.
CC TITLE OF INVENTION: RECEPTOR PROTEINS
RESULT 5
ID US-08-149-105-15 STANDARD; PRT; 501 AA.
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AC xxxxxx
XX

DT	01-JAN-1900	CC	APPLICANT: Ib ez, Carlos F.	CC	APPLICANT: Ryd n, Mikael	CC	APPLICANT: J rnvall, Henrik	CC	TITLE OF INVENTION: A No. 5614609el Serine Threonine Kinase Receptor	CC	NUMBER OF SEQUENCES: 6	CC	CORRESPONDENCE ADDRESS:	CC	ADDRESS: Sterne, Kessler, Goldstein & Fox	CC	STREET: 1100 New York Avenue, Suite 600	CC	CITY: Washington	CC	STATE: DC	CC	COUNTRY: USA	CC	ZIP: 20005	CC	COMPUTER READABLE FORM:	CC	MEDIUM TYPE: Floppy disk	CC	COMPUTER: IBM PC compatible	CC	OPERATING SYSTEM: PC-DOS/MS-DOS	CC	SOFTWARE: PatentIn Release #1.0, Version #1.25	CC	CURRENT APPLICATION DATA:	CC	APPLICATION NUMBER: US/08/341.916	CC	FILING DATE: Herewith	CC	CLASSIFICATION: 514	CC	ATTORNEY/AGENT INFORMATION:	CC	NAME: Goldstein, Jorge A.	CC	REGISTRATION NUMBER: 29,021	CC	REFERENCE/DOCKET NUMBER: 1459.0230001	CC	TELECOMMUNICATION INFORMATION:	CC	TELEPHONE: (202)371-2606	CC	TELEFAX: (202)371-2540	CC	INFORMATION FOR SEQ ID NO: 2:	CC	SEQUENCE CHARACTERISTICS:	CC	LENGTH: 493 amino acids	CC	TYPE: amino acid	CC	TOPOLOGY: linear	CC	MOLECULE TYPE: protein	CC	SEQUENCE 493 AA; 54800 MW; 1225231 CN;	CC	Query Match 64.7%; Score 2384; DB 6; Length 493;	CC	Best Local Similarity 68.3%; Pred. 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ALK-6

MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
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Tabular output not generated. 1344.779 Million cell updates/sec

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Description: (1-1952) from US08436265.seq
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N.A. Sequence: 1 AAGCGCGGAGAGTTCGCC.....CCATTTTTTATAAAAAA 1952
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Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 333249 seqs, 555961234 bases x 2

Processing: Minimum Match 0%
Listing first 45 summaries

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9:INV3 10:INV4 11:INV5 12:INV6 13:INV7 14:ORG 15:MAM
16:VRT 17:PLN 18:PRO1 19:PRO2 20:ROD 21:SYN 22:UNC
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1175:V

REFERENCE 2 (bases 1 to 2252)
AUTHORS Sumitomo,S., Saito,T. and Nohno,T.
TITLE A new receptor protein kinase from chick embryo related to type II receptor for TGF-beta
JOURNAL DNA Sequence 3, 297-302 (1993)
MEDLINE 94003400
COMMENT Submitted (20-OCT-1992) to DDBJ by: Teutomu Nohno
Department of Pharmacology
Kawasaki Medical School
577 Matsushima
Kurashiki 701-01
Japan
Phone: 086-462-1111

Query Match 47.8%; Score 933; DB 49; Length 2252;
Best Local Similarity 80.7%; Pred. No. 0.00e+00;
Matches 1227; Conservative 0; Mismatches 294; Indels 0; Gaps 0;

MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Jun 26 02:16:28 1997; MasPar time 188.32 Seconds
958.907 Million cell updates/sec

Tabular output not generated.

Description: >US-08-436-265-17
(1-1952) from US08436265.seq
Perfect Score: 1952
N.A. Sequence: 1 AACGGGGGCGAGAGTTGCC.....CCATTTTTTATAAAAAA 1952
Comp: TTGCGCCCGCTTCAACGG.....GGTAAAAAATATTTTTT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 121476 seqs, 46255616 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 9.725; Variance 5.247; scale 1.853

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1952	100.0	1952	16	T06032 Mouse ALK-6 cDNA.	0.00e+00
2	1948	99.8	1952	11	Q66642 Mouse Activin receptor	0.00e+00
3	1662	85.1	2076	14	Q83531 Sequence encoding bon	0.00e+00
4	937	48.0	2252	20	T27229 Bone morphogenetic pr	0.00e+00
5	933	47.8	2252	23	T28022 Chick BMP type I rece	0.00e+00
6	533	27.3	1813	14	Q83530 Sequence encoding bon	0.00e+00
7	522	26.7	2070	11	Q66640 Mouse Activin recepto	0.00e+00
8	520	26.6	2402	20	T27228 Bone morphogenetic pr	0.00e+00
9	520	26.6	2402	14	Q90184 BRK-1 DNA.	0.00e+00
10	520	26.6	2402	23	T28021 Mouse BMP type I rece	0.00e+00

RESULT 1
ID T06032 standard; cDNA; 1952 BP.
AC T06032;

DT 13-FEB-1996 (first entry)
DE Mouse ALK-6 cDNA.
KW ALK-6; OPI binding receptor; osteogenic protein 1; morphogenesis;
KW morphogen; agonist; antagonist; chimeric receptor; gene therapy; ss.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 187..1695
FT /tag= a
FT sig_peptide 187..252
FT /tag= b
FT mat_peptide 253..1692
FT /tag= c
FT /product= mouse ALK-6
PN W09530003-A2.
PD 29-NOV-1995.
PF 28-APR-1995; U05467.
PR 29-APR-1994; US-236428.
PA (CREA-) CREATIVE BIOMOLECULES INC.

RESULT 2

ID Q66642 standard; cDNA; 1952 BP.
AC Q66642;
DT 20-JAN-1995 (first entry)
DE Mouse Activin receptor-like kinase 6 (mALK-6) cDNA.
KW serine threonine kinases; activin receptors; Act-R; superfamily;
KW transforming growth factor; TGF; diagnostics; detection; therapy;
KW rheumatoid arthritis; glomerular nephritis; fibrosis; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT 5'UTR 1..186
FT /tag= a
FT /note= "contains an in-frame stop codon at nucleotides 163-165"
FT CDS 187..1695
FT /tag= b
FT /product= activin receptor-like kinase 6
FT 3'UTR 1696..1952
FT /tag= c
FT /note= "there is no polyA signal indicating that the cDNA was internally primed"

PN W09411502-A.
PD 26-MAY-1994.
PF 17-NOV-1993; G02367.
PR 17-NOV-1992; GB-024057.
PR 08-MAR-1993; GB-004677.
PR 08-MAR-1993; GB-004680.
PR 28-MAY-1993; GB-011047.
PR 02-JUL-1993; GB-013763.
PR 03-AUG-1993; GB-016099.
PR 15-OCT-1993; GB-021344.
PA (LUDW-) LUDWIG INST CANCER RES.
PI DiJke P, Franzen P, Heldin C, Miyazono K, Yamashita H;
DR WPI; 94-183503/22.
DR P-PSDB; R55374.

Query Match

Best Local Similarity 99.8%; Score 1948; DB 11; Length 1952;
Matches 1950; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 3

ID Q83531 standard; DNA; 2076 BP.
AC Q83531;
DT 28-SEP-1995 (first entry)
DE Sequence encoding bone morphogenic protein receptor CFK1-43a.
KW Bone morphogenic protein; receptor; serine/threonine kinase; BMP;
KW bone; cartilage; injury; treatment; inhibition; ss.
OS Rattus rattus.
FH Key Location/Qualifiers
FT CDS 247..1755
FT /tag= a

/product= Bone morphogenic protein receptor.
 PN W09507982-A.
 PD 23-MAR-1995.
 PF 07-SEP-1994; U10080.
 PR 17-SEP-1993; US-123934.
 PI (GEMV) GENETICS INST INC.
 PA Celeste AJ, Thies RS, Wozney JM, Yamaji N;
 DR WPI; 95-131350/17.
 DR P-PSDB; R70238.
 PR Truncated BMP and serine/threonine kinase receptor proteins -
 PT used to inhibit the effects of BMP-2 and/or BMP-4.
 PS Claim 2; Page 52-54; 83pp; English.
 CC Truncated bone morphogenic protein (BMP) receptors and
 CC serine/threonine kinase receptors may be used in compositions to
 CC inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated
 CC receptors pref. comprise the ligand binding domain, but not the
 CC serine/threonine kinase and transmembrane domains. The truncated
 CC proteins are soluble and will be excreted into supernatant by
 CC recombinant mammalian cells expressing them. Such cells can be
 CC delivered in a medium or matrix which partially impedes their
 CC mobility, thereby localising the cells to a site of bone or
 CC cartilage injury.
 SC Sequence 2076 BP; 598 A; 481 C; 527 G; 470 T;

141 aactcggctgaatcaaacaccattggcgctgagctatgacagagcaaacaaaagt 200
 80 AAC:TCGGCTGAATCACAACATTTGGCGCTGAGCTATGACAAAGAGACAAACAAAAGT 139
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 200 GCTCTGGAATAAATTGCTGGGCAACGAAGAGGATGGAGAGTAGACAGCCCCCACCC 259
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 Qy 1280 ACATCCCAACCAACACCCGGTGGCACCAAGCGCTATATGCTCCAGAAGTGTCTGGAAGC 1339
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 Qy 1340 AGAGCTTGAATAGAAACCATTTCCAGTCTTACATTATGGCTGACATGTACAGCTTTGGAC 1399
 Db 1460 tcatcctctgggagatgtcgaagagatgtgttcttgaggtatagtggagaataccagc 1519
 Qy 1400 TCATCTCTGGGAGATTCAAGAGAGATGTGTTTCTGGAGGTATAGTGGAGAATACACAGC 1459
 Db 1520 ttccatatcagacactgtgcccagtgacccctcttatgaggacatgagagaaatctgtg 1579
 Qy 1460 TTCCCTTATCAGCACTGTGTGCCAGTGACCCCTTCTTATGAGGACATGAGAGAAATTTGTG 1519
 Db 1580 gtatgaagaagtacggccttccatccccaatcgatggagcagtgacgagtgccctcaggc 1639
 Qy 1520 GCATGAAGAAATTTACGGCTTCAATTCCTCCCAATCGATGAGCAGTGTAGTGTCTCAGGC 1579
 Db 1640 aaatggggaagcttatgacagagtgctgggcgcataaatcctgctccaggtcgacggccc 1699
 Qy 1580 AGATGGGAAGCTTATGACAGAGTGTGGCGCAGAAATCCTGCTCCAGGCTGACGGCCC 1639
 Db 1700 tgagagttaaagaaacacttgcctcctcagagtgcccaggaatcctcctcctgacgtc 1759
 Qy 1640 TGAGAGTTAAGAAACCCCTTGCCAAAATGTACAGTCCCAGGACATTAACATCTTGACGTC 1699
 Db 1760 aggtactgtggacagagcaagcaattacacagaagcattccttagcccaagccttgaaag 1819
 Qy 1700 AGATACTTGTGGACAGAGCAAG-AATTTACAGAAGCATCGTTAGTCCCAAGCCTTGAACG 1758
 Db 1820 ttctactctgcccagtgagttcagacttctcctcctcctcctcctcctcctcctcctcctc 1879
 Qy 1759 TTAGCCTACTGCCAGTGAGTTTACAGCTTCTCTGGAAGAGACGCGTGGGCGAGACACAG 1818

Db	1880	aggaacccagaaaacacgcttccaccatggtcttctgagagggggaaccatttgggtaac	1939
Qy	1819	AGGAACCCAGAAACACGGATTATCATGGCTTTCTGAGGAGGAGAACTGTTTGGETAAC	1878
Db	1940	ttgttcaagatatgatgcattgctctcttctaagaaagccctgtattttggattaccatt	1999
Qy	1879	TTGTTCAAGATATGATGCATGTTGCTTCTTAAGAAAGCCTGTATTTTGA-ATTACCATT	1937
Db	2000	ttttttcaagaagaa	2014
Qy	1938	TTTTTATAAAAAAA	1952

MPsrch	nn	n.a.	-	n.a.	database search,	using Smith-Waterman algorithm

Run on: Thu Jun 26 02:25:10 1997; MasPar time 1244.32 Seconds

```

Title:
Description:
Perfect Score:
Seq:
1 AAGCGGCGGCAGAAAGTTGCC.....CCATTTTTTTTATAAAAAAAA 1952
TTCGCGCGCGTCTTCAACGG.....GGTAAAAAATAATTTTTTTT
Comp:

```

Scoring table: TABLE default

Nmatch STD : Dbase 0; Query 0

Searches: 320523884 bases x 3
- 87282 seqs.

Post-processing: -Minimum Match 0%
-Listing first 45 summaries

Database: EST-STS

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	295	15.1	471	164	mc33h08.r1 Soares mou	0.00e+00
2	200	10.2	404	165	zc18g04.r1 Soares par	0.00e+00
3	144	7.4	739	231	zf53c07.r1 Soares ret	4.23e-27
4	144	7.4	739	231	zf53c07.r1 Soares ret	4.23e-275
5	132	6.8	259	38	EST109182 Rattus sp.	2.26e-245
6	126	6.5	515	43	Human placenta cDNA 5	1.33e-230
7	126	6.5	515	239	Human placenta cDNA 5	1.33e-23
8	122	6.2	631	168	mc85f09.r1 Soares mou	8.53e-22
9	93	4.8	354	63	H. sapiens partial cd	7.43e-151
10	92	4.7	343	103	yg20f06.r1 Homo sapie	1.73e-14

1	RESULT	LOCUS	471 bp	mRNA	EST	11-SEP-1996
	DEFINITION	mc3h3h08_r1 Soares mouse p3NNF19.5 Mus musculus cDNA clone 350367 5' similar to gb:Z22535_cds1 SERINE/THREONINE-PROTEIN KINASE RECEPTOR R5 PRECURSOR (HUMAN); gb:Z23143 M.musculus ALK-6 mRNA, complete CDS (MOUSE) ;				

ACCESSION	W34981	DATE	1977
NID	G1316900		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		

Miss:

REFERENCE
AUTHORS
1 (bases 1 to 471)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steotje, M., Tan, F., Underwood, K., Moore, B.,

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	1952	100.0	1952	11	PCT-US95-0	Sequence 7, Applicatio	0.00e+00
2	1664	85.2	2076	10	PCT-US94-1	Sequence 3, Applicatio	0.00e+00
3	533	27.3	1813	10	PCT-US94-1	Sequence 1, Applicatio	0.00e+00
4	508	26.0	2932	11	PCT-US95-0	Sequence 5, Applicatio	0.00e+00
5	263	13.5	1647	10	PCT-US94-1	Sequence 7, Applicatio	2.72e-197
6	252	12.9	1506	5	US-08-317-	Sequence 4, Applicatio	1.99e-196
7	252	12.9	1506	5	US-08-317-	Sequence 2, Applicatio	8.55e-188
8	252	12.9	1506	5	US-08-149-	Sequence 2, Applicatio	8.55e-188
9	252	12.9	1506	5	US-08-149-	Sequence 4, Applicatio	8.55e-188
10	252	12.9	1506	5	ALIGNMENTS		

RESULT 1
ID PCT-US95-05467-7 STANDARD; DNA; UNC; 1952 BP.

AC XXXXXX
DT 01-JAN-1900
DE Sequence 7, Application PC/TUS9505467.
CC Sequence 7, Application PC/TUS9505467
CC GENERAL INFORMATION:
CC APPLICANT:
CC APPLICANT:
CC TITLE OF INVENTION: MORPHOGENIC PROTEIN-RECEPTOR CELL
CC TITLE OF INVENTION: SURFACE RECEPTORS AND USES THEREFOR
CC NUMBER OF SEQUENCES: 15

RESULT 2
ID PCT-US94-10080-3 STANDARD; DNA; UNC; 2076 BP.

AC XXXXXX
DT 01-JAN-1900
DE Sequence 3, Application PC/TUS9410080.
CC Sequence 2, Application PC/TUS9410080
CC GENERAL INFORMATION:
CC APPLICANT: GENETICS INSTITUTE, INC.
CC TITLE OF INVENTION: RECEPTOR PROTEINS
CC NUMBER OF SEQUENCES: 19
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: Genetics Institute Inc.- Legal Affairs
CC STREET: 87 CambridgePark Drive
CC City Match
CC Local Similarity 94.8%; Pred. No. 0.00e+00; Length 2076;
Matches 1777; Conservative 0; Mismatches 95; Indels 3; Gaps 3;

Db	141	AACITCGGCTGAATCAACACCAATTTGGCGTGAGCTATGACACAGAGAGCAACAAAAAGT	200
Qy	80	AACITCGGCTGAATCAACACCAATTTGGCGTGAGCTATGACACAGAGAGCAACAAAAAGT	139
Db	201	TAAAGGAGCAACTCGGCCCAATAGTGAC-AGAGAAGTTCGTTGATAACATGCTCTTACGAA	259
Qy	140	TAAAGGAGCAACCCGCCCAATAGTGAAGAGAGAGTTTATTGATAACATGCTCTTACGAA	199
Db	260	GCTCTGGAAAATTAAATGTGGGCACCAAGAGGAGATGGTGAGAGTACAGCCCCCACTG	319
Qy	200	GCTCTGGAAAATTAAATGTGGGCACCAAGAGGAGATGGTGAGAGTACAGCCCCCACTG	259
Db	320	CTCGGCCCAAGTCTCGGTTGTAATGCCACCACTGTCTCTGGAAGACTCAGTCAACA	379
Qy	260	CTCGGCCCAAGTCTCGGTTGTAATGCCACCACTGTCTCTGGAAGACTCAGTCAACA	319
Db	380	ATATCTGAGCAGATGGGTACTGCTTCACGATGATAGAGAAGACGACTCTGGAACGC	439
Qy	320	ATATCTGAGCAGATGGGTACTGCTTCACGATGATAGAGAAGACGACTCTGGAATGC	379

PD 23-MAR-1995.
 PF 07-SEP-1994; U10080.
 PR 17-SEP-1993; US-123934.
 PA (GEM) GENETICS INST INC.
 PI Celeste AJ, Thies RS, Wozney JM, Yamaji N;
 DR WPI; 95-131350/17.
 DR N-PSDB; Q83531.
 PT Truncated BMP and serine/threonine kinase receptor proteins -
 PT used to inhibit the effects of BMP-2 and/or BMP-4.
 PS Claim 17; Page 54-55; 83pp; English.
 CC Truncated bone morphogenic protein (BMP) receptors and
 CC serine/threonine kinase receptors may be used in compositions to
 CC inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated
 CC receptors pref. comprise the ligand binding domain, but not the
 CC serine/threonine kinase and transmembrane domains. The truncated
 CC proteins are soluble and will be excreted into supernatant by
 CC recombinant mammalian cells expressing them. Such cells can be
 CC delivered in a medium or matrix which partially impedes their
 CC mobility, thereby localising the cells to a site of bone or
 CC cartilage injury.
 CC Sequence for AA;
 SQ

Query Match 99.2%; Score 3711; DB 13; Length 502;
 Best Local Similarity 99.0%; Pred. No. 0.00e+00;
 Matches 497; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 1 mlrsgskinvgtkckgedestaprkpvkckchhpcdsnmicstgdyuftmleed 60
 1 MLLRSSGKLVGTVKCKEDGESTAPRPKILRCKCHHCPEDSVNNICSTGDCYFTMIEED 60
 61 dsgrpvtsgclglegsdfoqrdrtpipqhrrsieccternecndkhlptlpkldrdvfd 120
 61 DSGMPVVTSGCLGLEGSDFOQRDRTPIPQHRRSIECCTERNECNKDHLPTLPKLDKRDVFD 120
 121 gpihhkallsvtvcslvllvliifcyfrykrqearprysigleqdetyippgeslrdli 180
 121 GPIHHKALLISVTVCSLLVLLIIFCYFRYKRQEARPRYSIGLEQDETYIPPGESLRDLI 180
 181 eqsgsgsgglpllvqrtiakqimvkgigkrygevmgkwrgkvavkvfftteas 240
 181 EQSQSSGSGGLPLLVQRTIAKQIMVKIGKRYGEVVMGKWGRGEKAVKVFFTTTEAS 240
 241 wfretetiqtvlmrhenilgfiaadikgtgswtqllyitdyhengslvdyklttdaks 300
 241 WFRETEIYQTVLMRHNILGFIAADIKGTGSWTQLYLTIDYHENGSLVDYKLTTLDAKS 300
 301 mklayssvsglchlhteftstgkpaiahrdlksnilykngtcciadlglavkfisd 360
 301 MKLAYSSVSGLCHLHTEIFSTQKPAIAHRDLKSNILYKNGTCCCIADLGLAVKFISD 360
 361 tnevdiptnrvgtkrymppevldeslnrthfgsyimadmysfgllilweiarrcvsggiv 420
 361 TNEVDIPNTRVGTKRYMPPEVLDESINRTHFGSYIMADMYSFGLILWEIARRCVSGGIV 420
 421 eeyqlpyhdlvpsdpsyedmrreivcmkklrpsfnpnrwssdeclrmgklmtecwahnps 480
 421 EEQQLPYHDLVPSDPSYEDMRREIVCMKKLRPSFNPNRWSSDECLRMGKLMTECWAHPAS 480
 481 rltalrvkktlakmsesqdikl 502
 481 RLTAALRVKKTAKMSESQDIKL 502
 RESULT 4
 ID R95226 standard; Protein; 502 AA.
 AC R95226;
 DT 31-DEC-1996 (first entry)
 DE Chick BMP type I receptor kinase protein (BRK-2).
 KW BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein;
 KW BMP type I receptor kinase; BRK-2; BMP receptor.
 OS Gallus sp.

PN W09614579-A1.
 PD 17-MAY-1996.
 PF 30-OCT-1995; U14027.
 PR 04-NOV-1994; US-334178.
 PA Celeste AJ, Thies RS, Wozney JM, Yamaji N;
 DR WPI; 95-131350/17.
 DR N-PSDB; Q83531.
 PT Truncated BMP and serine/threonine kinase receptor proteins -
 PT used to inhibit the effects of BMP-2 and/or BMP-4.
 PS Claim 17; Page 54-55; 83pp; English.
 CC Truncated bone morphogenic protein (BMP) receptors and
 CC serine/threonine kinase receptors may be used in compositions to
 CC inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated
 CC receptors pref. comprise the ligand binding domain, but not the
 CC serine/threonine kinase and transmembrane domains. The truncated
 CC proteins are soluble and will be excreted into supernatant by
 CC recombinant mammalian cells expressing them. Such cells can be
 CC delivered in a medium or matrix which partially impedes their
 CC mobility, thereby localising the cells to a site of bone or
 CC cartilage injury.
 CC Sequence for AA;
 SQ

Query Match 92.7%; Score 3466; DB 19; Length 502;
 Best Local Similarity 91.6%; Pred. No. 0.00e+00;
 Matches 460; Conservative 23; Mismatches 19; Indels 0; Gaps 0;
 1 mlrsgskinvgtkckgedestaprkpvkckchhpcdsnmicstgdyuftmleed 60
 1 MLLRSSGKLVGTVKCKEDGESTAPRPKILRCKCHHCPEDSVNNICSTGDCYFTMIEED 60
 61 dsgrpvtsgclglegsdfoqrdrtpipqhrrsieccternecndkhlptlpkldrdvfd 120
 61 DSGMPVVTSGCLGLEGSDFOQRDRTPIPQHRRSIECCTERNECNKDHLPTLPKLDKRDVFD 120
 121 gpihhkallsvtvcslvllvliifcyfrykrqearprysigleqdetyippgeslrdli 180
 121 GPIHHKALLISVTVCSLLVLLIIFCYFRYKRQEARPRYSIGLEQDETYIPPGESLRDLI 180
 181 eqsgsgsgglpllvqrtiakqimvkgigkrygevmgkwrgkvavkvfftteas 240
 181 EQSQSSGSGGLPLLVQRTIAKQIMVKIGKRYGEVVMGKWGRGEKAVKVFFTTTEAS 240
 241 wfretetiqtvlmrhenilgfiaadikgtgswtqllyitdyhengslvdyklttdaks 300
 241 WFRETEIYQTVLMRHNILGFIAADIKGTGSWTQLYLTIDYHENGSLVDYKLTTLDAKS 300
 301 mklayssvsglchlhteftstgkpaiahrdlksnilykngtcciadlglavkfisd 360
 301 MKLAYSSVSGLCHLHTEIFSTQKPAIAHRDLKSNILYKNGTCCCIADLGLAVKFISD 360
 361 tnevdiptnrvgtkrymppevldeslnrthfgsyimadmysfgllilweiarrcvsggiv 420
 361 TNEVDIPNTRVGTKRYMPPEVLDESINRTHFGSYIMADMYSFGLILWEIARRCVSGGIV 420
 421 eeyqlpyhdlvpsdpsyedmrreivcmkklrpsfnpnrwssdeclrmgklmtecwahnps 480
 421 EEQQLPYHDLVPSDPSYEDMRREIVCMKKLRPSFNPNRWSSDECLRMGKLMTECWAHPAS 480
 481 rltalrvkktlakmsesqdikl 502
 481 RLTAALRVKKTAKMSESQDIKL 502
 RESULT 5
 ID R96202 standard; Protein; 502 AA.
 AC R96202;

22-AUG-1996 (first entry)
Bone morphogenetic protein type-1 receptor kinase-2.
Chicken; bone morphogenetic protein kinase-2;
bone morphogenetic protein kinase-3; antibody; diagnostic;
bone disorder; osteogenic; bone morphogenetic protein-agonist;
drug screening; reporter gene; bone morphogenetic protein-antagonist;
hormone-responsive element.
Gallus domesticus.
Key Location/Qualifiers
FT Peptide 186..191
FT /note= "Conserved BRK-2 motif"
PN WO9614412-A2.
PD 17-MAY-1996.
PF 30-OCT-1995; U14085.
PR 04-NOV-1994; US-7:1179.
PA (PROC) PROCTER & GAMBLE CO.
PI Nohno T, Rosenbaum JS;
DR WPI; 96-251762/25.
DR N-PSDB; T27229.
PT Isolated bone morphogenetic protein receptor kinase protein - used to
determine if a test cpd. is capable of binding to, or is
PT (ant)agonist of BMP receptor kinase protein transcription
PS Example 4; Page 67-68; 87pp; English.
CC The sequence represents chicken bone morphogenetic protein (BMP)
CC receptor type-I kinase-2 (BRK-1), which induces cellular
CC differentiation, response to BMP. Complex formation between
CC BRK-2 and type-I BRK-3 may be studied by co-expression of both
CC genes, followed by screening with an antibody generated against an
CC intracellular kinase peptide sequence present in BRK-1. BRK-2
CC contains an SCGSGS motif in the juxtamembrane region, 35-40 amino
CC acids from the transmembrane region, and the C-terminal region is
CC very short. The extracellular domain contains a cluster of
CC cysteine residues (cysteine box) within 25-30 amino acids of the
CC transmembrane region, and an upstream cysteine box after the
CC putative signal peptide. The BRK-3 receptor and antibodies against
CC it may be used in diagnostic assays for BMP disorders, or in
CC therapy to bind or scavenge BMPs. In addition, expression of the
CC BRK-3 gene along with a reporter gene under the control of a
CC hormone- responsive element in a cell culture may be used to screen
CC compounds for BRK-agonist or -antagonist activity, by monitoring
CC reporter gene expression.
SQ Sequence - 502 AA;

Query Match 92.7%; Score 3466; DB 17; Length 502;
Best Local Similarity 91.6%; Pred. No. 0.00e+00;
Matches 460; Conservative 23; Mismatches 19; Indels 0; Gaps 0;
1 mp1lsssklsmesrkedsegatpappqkklscqhhchpcdsnstcstgdcyftieed 60
1 MLLRSSGKLVNVTGKEDGESTAPTPRPKILRCKHHCHPCDSVNNICSTDGICYFTMIEE 60
61 dsghlvkcg1glegsfqcrdtpipqrrsiectgqdycknhlhtlplknrdfae 120
61 DSGMPVVTSGCLGEGSDFOCRTDTPIPQRRSIECTERNECNKDLHTLPLPKDRDFVD 120
121 gnhhkallsvtvcsllylilifcyfrykrqearprysigleqdetypggeslkdl 180
121 GPIHHKALLISVTVCSLLVLIILFCYFRYKRQEARPRYSIGLEQDETYIPPGESLRDLI 180
181 eqsssgsgsglpllvqrtiakqimvrgkqgrgyevwmkgvavkvfftteas 240
181 EQSSSGSGSGGLPLLQVQRTIAKQIMVQIGKGRYGEVWMGKRGKAVKVVFFTTTEAS 240
241 wfreteiyqvtvlmrhenilgfiaadikgtgswtqllyitdyhengsllydylkstldtkg 300
241 WFRETEIYQVTVLMRHENILGFIAADIKGTGWSWTQLYLIITDYHENGSLYDYLKSTLDAKS 300
301 mlklayssvg1chlhtgftgqkpaiahrdlksknilylkkngtcciadlglavkfisd 360
301 MLKLAYSSVSG1CHLHTGFTGQKPAIAHRLDKSKNIIYLLKKNGTCCIAIDLGLAVKFI 360

Db 361 tnevdiptnrvgtkrymppevldeslnrhfgsyimadmysfglilweiarrcvsgiv 420
Qy 361 TNEVDIPPTNTRVGTGRYMPPEVLDSELNRRHFQSYIMADMYSGLLIWEIARRCVSGIV 420
Db 421 eeyqlpvhdlvpdspsvedmreivcikliirpsfnrswsdeclrmgklmmecwahnps 480
Qy 421 EYQLPVDHLPVPSDPSVEDMREIVCMKLRPFNPNRWSDECLRQMGKLMTECWAQNPAS 480
Db 481 rltalrvkktlakmsesqdikl 502
Qy 481 RLTAIRVKKTLAKMSESDIKL 502
RESULT 6
ID R85207 standard; Protein; 532 AA.
AC R85207;
DT 13-FEB-1996 (first entry)
DE Human ALK-3.
KW ALK-3; OPl binding receptor; osteogenic protein 1; morphogenesis;
KW morphogen; agonist; antagonist.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Sig_peptide
FT Domain 24..152
FT /label= Extracellular domain
FT Domain 153..235
FT /label= Transmembrane domain
FT Domain 236..527
FT /label= Intracellular domain
FT /note= "serine/threonine-kinase domain"
PN WO9614412-A2.
PD 09-JAN-1995.
PF 28-APR-1995; U05467.
PR 29-APR-1994; US-236428.
PA (CREA-) CREATIVE BIOMOLECULES INC.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Dijke PT, Heidin C, Miyazano K, Sampath KT;
DR WPI; 95-393076/50.
DR N-PSDB; T06031.
PT Identifying osteogenic protein-1 receptor-binding analogue - useful
PT in the design of morphogen agonists and antagonists for therapeutic,
PT diagnostic and experimental purposes
PS Claim 1; Page 68-71; 95pp; English.
CC The Type-1 cell surface receptors ALK-2, ALK-3 and ALK-6 (given in
CC R85206, R85207 and R85209) have specific binding affinity for
CC osteogenic protein 1 (OP1) and OP1-related analogues. The
CC receptors are used to identify novel morphogen receptor binding
CC analogues useful in drug design.
SQ Sequence 532 AA;

Query Match 73.7%; Score 2757; DB 14; Length 532;
Best Local Similarity 71.9%; Pred. No. 3.32e-259;
Matches 363; Conservative 76; Mismatches 61; Indels 5; Gaps 5;
29 mlhgtgmksddgkksengvtlapdtpflkcyccghchpcddainntcithghcfaiiee 88
2 LLRSSG-KLVNVTGK-EDGESTAPTPRPKILRCKHHCHPCDSVNNICSTDGICYFTMIEE 59
89 ddqgettlasgcmkyegsfqcdspkaqlrtieccrt-nlcnqylqtlppvvigpff 147
60 DSGMPVVTSGCLGEGSDFOCRTDTPIPQRRSIECTERNECNKDLHTLPLPKDRDFV 119
148 dgsirwlvllismavciamiifscfkykhyckysissrrrynrdledaeafipvgeslk 207
120 DGIPIHHKALLISVTVCSLLVLIIL-FCYFRY-KRQEARPRYSIGLEQDETYIPGESLR 177
208 dliagsqsgsgsglpllvqrtiakqimvrgkqgrgyevwmkgvavkvfftte 267
178 DLIEQSSSGSGSGGLPLLQVQRTIAKQIMVQIGKGRYGEVWMGKRGKAVKVVFFTTTE 237
268 easwfreteiyqvtvlmrhenilgfiaadikgtgswtqllyitdyhengsllydylkcatid 327

DATE 19-May-1994 #sequence_revision 19-May-1994 #text_change
ACCESSIONS 08-Dec-1995
REFERENCE A53444; S40159
#authors ten Dijke, P.; Yamashita, H.; Ichijo, H.; Franzen, P.; Laiho, M.; Miyazono, K.; Heldin, C.H.
#journal Science (1994) 264:101-104
#title Characterization of type I receptors for transforming growth factor-beta and activin.
#accession A53444
##status Preliminary
##molecule_type mRNA
##residues 1-502 ##label TEN
##cross-references GB:223143
REFERENCE S40159
#authors Miyazono, K.; Koren, A.; Grimsby, S.; Ichijo, H.; Heldin, C.; ten Dijke, P.
#submission submitted to the EMBL Data Library, June 1993
#description ALK-3 and ALK-6: the closely related members in the serine/threonine kinase receptor family.
#accession S40159
##status Preliminary
##molecule_type mRNA
##residues 1-502 ##label MIY
##cross-references EMBL:223143
CLASSIFICATION #superfamily protein kinase homolog;
FEATURE
202-498 #domain protein kinase homology #label KIN
SUMMARY #length 502 #molecular-weight 56944 #checksum 5099
Query #length 100.0%; Score 3740; DP 14; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
ENTRY JC2491 #type complete
TITLE serine/threonine kinase receptor - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 05-Jan-1996
ACCESSIONS JC2491
REFERENCE JC2491
#authors Yamaji, N.; Celeste, A.J.; Thies, R.S.; Song, J.J.; Bernier, S.M.; Goltzman, D.; Lyons, K.M.; Nove, J.; Rosen, V.; Wozney, J.M.
#journal Biochem. Biophys. Res. Commun. (1994) 205:1944-1951
#title A mammalian serine/threonine kinase receptor specifically binds BMP-2 and BMP-4.
#accession JC2491
##molecule_type mRNA
##residues 1-502 ##label YAM
CLASSIFICATION #superfamily protein kinase homology
KEYWORDS glycoprotein; transmembrane protein
FEATURE
127-148 #domain transmembrane #status predicted #label TMW
202-498 #domain protein kinase homology #label KIN
210-218 #region protein kinase ATP-binding motif
284,343,388 #binding_site carbohydrate (Asn) (covalent) #status predicted
SUMMARY #length 502 #molecular-weight 56870 #checksum 5258
Query Match 99.2%; Score 3711; DP 14; Length 502;
Best Local Similarity 99.0%; Pred. No. 0.00e+00;
Matches 497; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 3
ENTRY A56683 #type complete
TITLE receptor protein kinase RPK-1 precursor - chicken
ORGANISM #formal_name Gallus gallus #common_name chicken

Qy 238 EASWRETEIYQVLMRHENILGFIAADIKGTGWSQTLVLYITDYHENGSLYDLKSTTLD 297
Db 328 trallklaysaacglchlhtreiygtqgkpaiahrdlksnllkkngsecciadlglavkf 387
Qy 298 AKSWMLKLAYSSVGLCHLHTEIFSTQKPAIAHRDLKSNILVKNKGTCCTIADLGLAVKF 357
Db 388 nsdtnevdpvlntrvgtkrymapelvdeslnknhfpymadiysfgliiwemarrcitg 447
Qy 358 ISDTNEVDIPPNTRVGTRKRYMPPEVLDSESLNHFQSYINADMYSGFLILWEIARRCVSG 417
Db 448 giveeyqlpyymvpsdpsyedmrevvcvkrllrpivsnrnwdsdeclravklmsecwahn 507
Qy 418 GIVEEYQLPYHDLPSPDPSYEDMREIVCMKKLRPSPFNWSSDCLRQMGKLMTECWAQN 477
Db 508 pasrltalrvkktlakmvesqgdvki 532
Qy 478 PASRLTALRVKKTAKMSQSODIKL 502

MSrcch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Jun 24 17:55:41 1997; MasPar time 18.27 Seconds
#output not generated.
Title: >US-08-436-265-18
Description: (1-502) from US08436265.pep
Perfect Score: 3740
Sequence: 1 MJLFSGKLNVTGKKEDGES.....TALRVKKTIAKVSQSODIKL 502
Scoring table: Gap 11

Searched: 89912 seqs, 28507787 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:annn1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev
Statistics: Mean 48.874; Variance 115.786; scale 0.422

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description Pred. No.
1	3740	100.0	502	14	A53444 activin receptor-lik 0.00e+00
2	3711	99.2	502	14	JC2491 serine/threonine kin 0.00e+00
3	3466	92.7	502	13	A56683 receptor protein kin 0.00e+00
4	2757	73.7	532	13	I37163 ALK-3 - human 0.00e+00
5	2757	73.7	532	13	S37183 ALK-3 protein - huma 0.00e+00
6	2756	73.7	532	14	JC2387 bone morphogenetic p 0.00e+00
7	2756	73.7	532	14	A56238 bone morphogenetic p 0.00e+00
8	2645	70.7	527	12	A54985 BMP receptor precurs 0.00e+00
9	2505	67.0	500	14	B56238 bone morphogenetic p 0.00e+00
10	1831	49.0	503	14	JC2061 transforming growth 1.25e-292
ALIGNMENTS					
RESULT 1	A53444	#type complete			
ENTRY	activin receptor-like kinase 6 precursor - mouse				
TITLE	#formal_name Mus musculus #common_name house mouse				
ORGANISM					

DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Dec-1995

ACCESSIONS A56683

REFERENCE A56683

#authors Sumitomo, S.; Saito, T.; Nohno, T.

#journal DNA Seq. (1993) 3:297-302

#title A new receptor protein kinase from chick embryo related to type II receptor for TGF-beta.

#accession A56683

##status preliminary

##molecule_type mRNA

##residues 1-502 #label SUM

##cross-references GB:D13432

CLASSIFICATION #superfamily protein kinase homology

phosphotransferase; transmembrane protein

KEYWORDS

202-498 #domain protein kinase homology #label KIN

SUMMARY #length 502 #molecular-weight 56766 #checksum 5555

Query Match. 92.7%; Score 3466; DB 13; Length 502;

Best Local Similarity 91.6%; Pred. No. 0.00e+00;

Matches 460; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

I 1 mplskskmesrkedsegatpappqkklscqchhpcdsvnstcdgycftlieed 60

QY 1 MLLRSSGKLNVGTTKX-EDGESTAPTRPKILRCCKCHHCPEDSVNNICSTDGVCFALEED 60

Db 61 dsgghlvckglqlegsfcdrtipphqrrsiecctggqcnkhlhptlpklnrdfae 120

QY 61 DSGMPVVTSGCLGLESGDFQCRDTPIPHQRRIECCCTERNECNKDLHPTLPKLRDFVD 120

Db 121 gnihzkallivsvsllvliifcyfrykrqearprysiglegdeyippgesjkdli 180

QY 121 GPIHKKALLISVTVCSLLVLIILFCYFRYKQEARPRYSIGLEQDEYIIPGESLRDLI 180

Db 181 eqsdsqsgsglpllvqvtiakqimvkgqkgrgygevmgkwrgkvavkvffteeas 240

QY 181 EQSSSGSGGLPLLVQRTIAKQIQMVKQIGRGYGEVMMGWKRGKAVKRVFFTEEAS 240

Db 241 wfreteiyqvtvlmrhenilgfiaadikgtgswtqlvltidyhengslydyksttdtkg 300

QY 241 WFRETEYQTVLMRHNILGFIADIKGTGSWTQLVLTIDYHENGSLYDYLKSTTLDAKS 300

Db 301 mlklayssvgclhlthgftstgqkpaiahrdlksknilykngtcciadlglavkfisd 360

QY 301 MLKLAYSSVSGCLHLTHETESTQKPAIAHRLDKSNILYKNGTCCCIADIGLAVKFISD 360

Db 361 tnevdiipntrvgtkrympbevldeslnrhfnqsyimadmysfgliilweiarrovsggiv 420

QY 361 TNEVDIPNTRVGTKRYMPBEVLDESILNRNHFQSYIMADMYSPGLILWEIARRCVSGGIV 420

Db 421 eeyqlpyhdlvpsdyedrmreivcivklrpfnpnwssdeclrqmglmmecwahnpas 480

QY 421 EEEYQLPYHDLVPSDPSYEDRMREIVCMKKLRPFNPNRWSDECLRQMGKLMTECWAQNPAS 480

Db 481 rltalrvkktlakmsesqdikl 502

QY 481 RLTLRVKKTAKMSESQDIKL 502

RESULT 4

ENTRY I37163 #type complete

TITLE ALK-3 - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996

ACCESSIONS I37163

REFERENCE I37161

#authors ten Dijke, P.; Ichijo, H.; Franzen, P.; Schulz, P.; Saras, J.; Toyoshima, H.; Heldin, C.H.; Miyazono, K.

#journal Oncogene (1993) 8:2879-2887

#title Activin receptor-like kinases: a novel subclass of cell-surface receptors with predicted serine/threonine kinase activity.

#cross-references MUID:93390967

#accession I37163

##status preliminary; translated from GB/EMBL/DBDJ

##molecule_type mRNA

##residues 1-532 #label RES

##cross-references EMBL:Z22535; NID:g402186; CDS_PID:g402187

SUMMARY #length 532 #molecular-weight 60201 #checksum 6778

Query Match 73.7%; Score 2757; DB 13; Length 532;

Best Local Similarity 71.9%; Pred. No. 0.00e+00;

Matches 363; Conservative 76; Mismatches 61; Indels 5; Gaps 5;

Db 29 mlkgtg;akdsdsgksgenvgtlapedtlpfikycycghcpddainntcincghcfaiee 88

QY 2 LLRSSG-KLVNVTXK-EDGESTAPTRPKILRCCKCHHCPEDSVNNICSTDGVCFTMEE 59

Db 89 ddsgettlagcmkyegsdfqcdskpkaqlrrtlieccrt-nlcngylqtlppvvgifff 147

QY 60 DDSGMPVVTSGCLGLESGDFQCRDTPIPHQRRIECCCTERNECNKDLHPTLPKLRDFV 119

Db 148 dgsirwlvlismavciailfsscfcykhycksissrrrynrdleqdeafipvgeslk 207

QY 120 DSGHKKALLISVTVCSLLVLIIL-FCYFRY-KRQEARPRYSICHEQDEYIIPPGSLR 177

Db 208 dliidsqsgsgglpllvqvtiakqimvkgqkgrgygevmgkwrgkvavkvfftte 267

QY 178 DLIEQSSSGSGGLPLLVQRTIAKQIQMVKQIGRGYGEVMMGWKRGKAVKRVFFTE 237

Db 268 easwifreteiyqvtvlmrhenilgfiaadikgtgswtqlvltidyhengslydylkcatld 327

QY 238 EASWIFRETEYQTVLMRHNILGFIADIKGTGSWTQLVLTIDYHENGSLYDYLKSTLD 297

Db 328 trallklaysaacglchlhteiygtgkpaiahrdlksknilykngtcciadlglavkf 387

QY 298 AKSMLKLAYSSVSGGLPLLVQRTIAKQIQMVKQIGRGYGEVMMGWKRGKAVKRVFF 357

Db 388 nsdtnedvplntrvgtkrymapevldeslnrhfnqsyimadmysfgliiwemarrcitg 447

QY 358 ISDTNEVDIPNTRVGTKRYMPBEVLDESILNRNHFQSYIMADMYSPGLILWEIARRCVSG 417

Db 448 giveeyqlpyynmpdsyedmrevvcvkrilprlrvnsdeclrvlklmsecwahn 507

QY 418 GIVEEYQLPYHDLVPSDPSYEDRMREIVCMKKLRPFNPNRWSDECLRQMGKLMTECWAQN 477

Db 508 pasrltalrvkktlakmvesqdvki 532

QY 478 PASRLTALRVKKTAKMSESQDIKL 502

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jun 24 17:54:36 1997; MasPar time 12.58 Seconds

846.231 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-265-18

Description: (1-502) from US08436265.pep

Perfect Score: 3740

Sequence: 1 MLLRSSGKLNVGTTKEDGES.....TALRVKKTAKMSESQDIKL 502

Scoring table: PAM 150

Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot34

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 50.508; Variance 87.156; scale 0.580

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1740	100.0	502	5	KIR6_MOUSE SERINE/THREONINE-PROT	0.00e+00
2	3466	92.7	502	5	KIR6_CHICK SERINE/THREONINE-PROT	0.00e+00
3	2757	73.7	532	5	KIR5_HUMAN SERINE/THREONINE-PROT	0.00e+00
4	2756	73.7	532	5	KIR5_MOUSE SERINE/THREONINE-PROT	0.00e+00
5	1842	49.3	501	5	KIR4_RAT SERINE/THREONINE-PROT	0.00e+00
6	1793	47.9	503	5	KIR4_HUMAN SERINE/THREONINE-PROT	0.00e+00
7	1700	45.5	505	5	KIR2_HUMAN SERINE/THREONINE-PROT	0.00e+00
8	1696	45.3	505	5	KIR2_RAT SERINE/THREONINE-PROT	0.00e+00
9	1679	44.9	509	5	KIR1_HUMAN SERINE/THREONINE-PROT	0.00e+00
10	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
11	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
12	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
13	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
14	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
15	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
16	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
17	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
18	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
19	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
20	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
21	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
22	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
23	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
24	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
25	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
26	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
27	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
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29	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
30	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
31	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
32	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
33	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
34	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
35	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
36	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
37	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
38	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
39	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
40	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
41	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
42	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
43	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
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46	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
47	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
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49	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
50	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
51	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
52	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
53	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
54	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
55	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
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57	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
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64	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
65	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
66	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
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75	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
76	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
77	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
78	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
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92	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
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94	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
95	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
96	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
97	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
98	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
99	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00
100	1669	44.6	509	5	KIR1_RAT SERINE/THREONINE-PROT	0.00e+00

FT SIGNAL 1 13 POTENTIAL.
FT CHAIN 14 502 SERINE/THREONINE KINASE RECEPTOR R6.
FT DOMAIN 14 126 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 127 148 POTENTIAL.
FT DOMAIN 149 502 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 204 494 PROTEIN KINASE.
FT NP_BIND 210 218 ATP (BY SIMILARITY).
FT BINDING 231 231 ATP (BY SIMILARITY).
FT ACT_SITE 332 332 BY SIMILARITY.
FT CARBOHYD 44 44 POTENTIAL.
SQ SEQUENCE 502 AA; 56766 MW; D404D2DB CRC32;

Query Match 92.7%; Score 3466; DB 5; Length 502;
Best Local Similarity 91.6%; Pred. No. 0.00e+00;
Matches 460; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

Db 1 mpllssklmeskedsegtpapqkklscqchhhcpedsvnstcdstgyoftiieed 60
Qy 1 MLLRSSGLNVGTTKEDGESTAPTPRKILRCKHHCHPCDSVNNICSTDGYCFTMEED 60
Db 61 dsqghlvtkgclglegsfqcrdtphgrsrscctgqdycknhlhtlplknrdfae 120
Qy 61 DSGMPVVTSGCLGEGSDFQCRDTPPHQRRSIECCTERNECNKDLHPTLPKDRDFVD 120
Db 121 gnhhkallisvtcsillvliifcyfrykrgearpysigleqdetvppgeslkdl 180
Qy 121 GPIHRRALLISVTCSILLVLIIFCYFRYKRGEARPYSIGLEQDETIPPGESLRDLI 180
Db 181 eqsgsgsgglpllvrtiakqimvkgigkrygvmmgkwrgkvavkvftteas 240
Qy 181 EQSGSGSGGLPLLVRTIAKIQMVKGIGKRYGVMMGKWGEKAVKVFTTEAS 240
Db 241 wfretelvtqlvmlrhenilgfiaadikgtgswtqlvliitdyhengsllydylksttldtkg 300
Qy 241 WRETETVQVLMRHNILGFIADIKGTGSWTQLVLIITDYHENGSLYDYLKSTTLDKAS 300
Db 301 mlklayssvsglchlhtgftstqgkpaiahrdlksknlvkvkngtcciadlglavkfisd 360
Qy 301 MLKLAYSSVSGLCHLHTGFTSTQGKPAIAHRLDLKSKNLVKKNGTCCCIADLGLAVKFISD 360
Db 361 tnevdiptnrvgtkrymppevldeslnrhfsymadmysfglielwiarvcsggiv 420
Qy 361 TNEVDIPNTRVGTKRYMPPEVLDLSNRNHFQSYIMADMYSGLIILWEIARRCVSGGIV 420
Db 421 eevqlpvhdlvpsdpsyedmeivcirkrlrpsfnrwsddclrgmgklmmecwahnps 480
Qy 421 EEVQLPVHDLVPSDFSYEDMEIVCMKRLRPSFNRWSSDECLRQMGKLMTECWAQNPS 480
Db 481 rtalrvkktlakmsesqdikl 502
Qy 481 RLTAALRVKKTAKMSESQDIKL 502

RESULT 3
ID KIR5_HUMAN STANDARD; PRT; 532 AA.
AC P36894;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE SERINE/THREONINE-PROTEIN KINASE RECEPTOR R5 PRECURSOR (EC 2.7.1.37)
DE (SKR5) (ACTIVIN RECEPTOR-LIKE KINASE 3) (ALK-3).
GN ACVRLK3
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
RX MEDLINE; 93390967.
RA TEN DIJKE P., ICHIO H., FRANZEN P., SCHULZ P., SARAS J.,
RA TOYOSHIMA H., HELDIN C.H., MIYAZONO K.;

Query Match 73.7%; Score 2757; DB 5; Length 532;
Best Local Similarity 71.9%; Pred. No. 0.00e+00;
Matches 363; Conservative 76; Mismatches 61; Indels 5; Gaps 5;
Distribution rights by Inteligenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu May 22 14:34:54 1997; MasPar time 4.68 Seconds
353.311 Million cell updates/sec
Tabular output not generated.

Title: >US-08-436-265-18
Description: (1-502) from US08436265.pep
Perfect Score: 3740
Sequence: 1 MLLRSSGLNVGTTKEDGES.....TALRVKKTIAKMSQSUIKL 502

Scoring table: PAM 150
Gap 11

Searched: 35845 seqs, 3290575 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-us08-436-265-18
1:51 2:52 3:53 4:54 5:55 6:PT90 7:PT91 8:PT92 9:PT93
10:PT94 11:PT95 12:PT96

Statistics: Mean 33.828; Variance 163.878; scale 0.206

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description	Pred. No.
1	3740	100.0	502	11	PCT-US95-0 Sequence 8, Applicatio	0.00e+00
2	3711	99.2	502	10	PCT-US94-1 Sequence 4, Applicatio	0.00e+00
3	2757	73.7	532	11	PCT-US95-0 Sequence 6, Applicatio	1.10e-229
4	2756	73.7	532	10	PCT-US94-1 Sequence 2, Applicatio	1.34e-229
5	1842	49.3	501	5	US-08-317- Sequence 17, Applicati	1.05e-148
6	1842	49.3	501	5	US-08-149- Sequence 17, Applicati	1.05e-148
7	1831	49.0	503	10	PCT-US94-1 Sequence 10, Applicatio	9.82e-148
8	1690	45.2	505	10	PCT-US94-1 Sequence 8, Applicatio	2.66e-135
9	1679	44.9	509	11	PCT-US95-0 Sequence 4, Applicatio	2.48e-134
10	1670	44.7	501	5	US-08-149- Sequence 15, Applicati	1.54e-133

RESULT 1
ID PCT-US95-05467-8 STANDARD; PRT; 502 AA.

XX AC

XX XX

XX 01-JAN-1900

DE Sequence 8, Application PC/TUS9505467.

XX Sequence 8, Application PC/TUS9505467.

CC GENERAL INFORMATION:

CC APPLICANT:

CC TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL

CC TITLE OF INVENTION: SURFACE RECEPTORS AND USES THEREFOR

RESULT 2

ID PCT-US94-10080-4 STANDARD; PRT; 502 AA.

AC xxxxxx

XX 01-JAN-1900

DE Sequence 4, Application PC/TUS9410080.

XX Sequence 4, Application PC/TUS9410080

CC GENERAL INFORMATION:

CC APPLICANT: GENETICS INSTITUTE, INC.

CC TITLE OF INVENTION: RECEPTOR PROTEINS

CC NUMBER OF SEQUENCES: 19

Query Match 99.2%; Score 3711; DB 10; Length 502;

Best Local Similarity 99.0%; Pred. No. 0.00e+00;

Matches 497; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db	1	MLLRSSGLNVGTTKEDGESTAPTARPKVLRKCHHHCPEDSVNNICSDGYCFTMEED	60
Qy	1	MLLRSSGLNVGTTKEDGESTAPTARPKVLRKCHHHCPEDSVNNICSDGYCFTMEED	60
Db	61	DSGTPVWTSCGLGEGSDFQCRDTPIPHQRRTIECCTERNECNKDLHPTLPKLDKDFVD	120
Qy	61	DSGMPVVTSCGLGEGSDFQCRDTPIPHQRRTIECCTERNECNKDLHPTLPKLDKDFVD	120
Db	121	GPVHKALLISVTVCSLLLVLLILFCYFRYKROEARPRYSIGLEODETYIPPGESLRDLI	180
Qy	121	GPVHKALLISVTVCSLLLVLLILFCYFRYKROEARPRYSIGLEODETYIPPGESLRDLI	180
Db	181	EOSQSSGSGSLPLLAVQRTIAKIQMVKQIGKRGYGEVMMGKRGKAVKVFVFTTEAS	240
Qy	181	EOSQSSGSGSLPLLAVQRTIAKIQMVKQIGKRGYGEVMMGKRGKAVKVFVFTTEAS	240
Db	241	WFRETEIYQTVLMRHNILGFIADIKGIGWTQLYLITDYHENGSLYDLKSTTLDKAS	300
Qy	241	WFRETEIYQTVLMRHNILGFIADIKGIGWTQLYLITDYHENGSLYDLKSTTLDKAS	300
Db	301	MLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRDLKSNILVKKNGTCCADLGLAVKFISD	360
Qy	301	MLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRDLKSNILVKKNGTCCADLGLAVKFISD	360
Db	361	TNEVDIPPNTRVGTKRYMPPEVLDLSNRTHFSYIMADWYSFGLILWEIARRCVSGGIV	420
Qy	361	TNEVDIPPNTRVGTKRYMPPEVLDLSNRTHFSYIMADWYSFGLILWEIARRCVSGGIV	420
Db	421	EYQLPYHDLVPSDPSYEDMREIVCMKKLRPSFPNRSWSSDECLRMGLMTECWAHPAS	480
Qy	421	EYQLPYHDLVPSDPSYEDMREIVCMKKLRPSFPNRSWSSDECLRMGLMTECWAHPAS	480
Db	481	RLTALRVKKTIAKMSQSODIKL 502	
Qy	481	RLTALRVKKTIAKMSQSODIKL 502	